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<110> Seishi KATO
 Chikashi EGUCHI
 Mihoro SAEKI

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Ser	Cys	Val	Glu
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Ile	Arg	Phe	Thr
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Val	Gly	Asn	Leu
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 Ser Ala Ala Pro Pro Gly Leu Glu Ala Ala Arg Gln Lys Leu Ala Leu
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cgg cgg aag aag gtg ctg agc acc gag gag atg gag ctg tac gag ctg 149
 Arg Arg Lys Lys Val Leu Ser Thr Glu Glu Met Glu Leu Tyr Glu Leu
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gcg cag gcg gcg ggc ggc gct atc gac ccc gac gtg ttc aag atc ctg 197
 Ala Gln Ala Ala Gly Gly Ala Ile Asp Pro Asp Val Phe Lys Ile Leu
 45 50 55

gtg gac ctg ctg aag ctg aac gtg gcc ccc ctc gcc gtc ttc cag atg 245
 Val Asp Leu Leu Lys Leu Asn Val Ala Pro Leu Ala Val Phe Gln Met
 60 65 70 75

ctc aag tcc atg tgt gcc ggg cag agg cta gcg agc gag ccc cag gac 293
 Leu Lys Ser Met Cys Ala Gly Gln Arg Leu Ala Ser Glu Pro Gln Asp
 80 85 90

cct gcg gcc gtg tct ctg ccc acg tcg agc gtg ccc gag acc cga ggg 341
 Pro Ala Ala Val Ser Leu Pro Thr Ser Ser Val Pro Glu Thr Arg Gly

95	100	105	
aga aac aaa ggc agc gct gcc ctc ggg gga gca ttg gcc ctg gcg gaa			389
Arg Asn Lys Gly Ser Ala Ala Leu Gly Gly Ala Leu Ala Leu Ala Glu			
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cgc agc agc cgc gaa gga tcc agc cag agg atg cca cgc cag ccc agc			437
Arg Ser Ser Arg Glu Gly Ser Ser Gln Arg Met Pro Arg Gln Pro Ser			
125	130	135	
gct acc agg ctg ccc aag ggg ggc ggg cct ggg aag agc cct aca cgg			485
Ala Thr Arg Leu Pro Lys Gly Gly Gly Pro Gly Lys Ser Pro Thr Arg			
140	145	150	155
ggc agc acc tag gatggggcag agacttggtg catctttgtc cccagcaaag			537
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35	40	45	
Gly Ala Ile Asp Pro Asp Val Phe Lys Ile Leu Val Asp Leu Leu Lys			
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Leu Asn Val Ala Pro Leu Ala Val Phe Gln Met Leu Lys Ser Met Cys			
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Ala Gly Gln Arg Leu Ala Ser Glu Pro Gln Asp Pro Ala Ala Val Ser			
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Leu Pro Thr Ser Ser Val Pro Glu Thr Arg Gly Arg Asn Lys Gly Ser			
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Ala Ala Leu Gly Gly Ala Leu Ala Leu Ala Glu Arg Ser Ser Arg Glu			
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Descriptive statistics		Descriptive statistics	
Variable	Mean	Variable	Mean
Age	34.5	Age	34.5
Gender	0.5	Gender	0.5
Marital status	0.5	Marital status	0.5
Education	12.5	Education	12.5
Income	15.5	Income	15.5
Health status	0.5	Health status	0.5
Employment status	0.5	Employment status	0.5
Home ownership	0.5	Home ownership	0.5
Auto ownership	0.5	Auto ownership	0.5
Life insurance	0.5	Life insurance	0.5
Disability insurance	0.5	Disability insurance	0.5
Health insurance	0.5	Health insurance	0.5
Retirement savings	0.5	Retirement savings	0.5
Charitable contributions	0.5	Charitable contributions	0.5
Gift giving	0.5	Gift giving	0.5
Travel expenses	0.5	Travel expenses	0.5
Entertainment expenses	0.5	Entertainment expenses	0.5
Food and beverage expenses	0.5	Food and beverage expenses	0.5
Utilities	0.5	Utilities	0.5
Transportation expenses	0.5	Transportation expenses	0.5
Medical expenses	0.5	Medical expenses	0.5
Education expenses	0.5	Education expenses	0.5
Other expenses	0.5	Other expenses	0.5
Total expenses	0.5	Total expenses	0.5
Net income	0.5	Net income	0.5
Assets	0.5	Assets	0.5
Liabilities	0.5	Liabilities	0.5
Net worth	0.5	Net worth	0.5
Financial health	0.5	Financial health	0.5
Overall financial well-being	0.5	Overall financial well-being	0.5

[illegible]

Descriptive statistics		Descriptive statistics	
Variable	Mean	Variable	Mean
Age	34.5	Age	34.5
Gender	0.5	Gender	0.5
Marital status	0.5	Marital status	0.5
Education	12.5	Education	12.5
Income	15.5	Income	15.5
Health status	0.5	Health status	0.5
Employment status	0.5	Employment status	0.5
Home ownership	0.5	Home ownership	0.5
Auto ownership	0.5	Auto ownership	0.5
Life insurance	0.5	Life insurance	0.5
Disability insurance	0.5	Disability insurance	0.5
Health insurance	0.5	Health insurance	0.5
Retirement savings	0.5	Retirement savings	0.5
Charitable contributions	0.5	Charitable contributions	0.5
Gift giving	0.5	Gift giving	0.5
Travel expenses	0.5	Travel expenses	0.5
Entertainment expenses	0.5	Entertainment expenses	0.5
Food and beverage expenses	0.5	Food and beverage expenses	0.5
Utilities	0.5	Utilities	0.5
Transportation expenses	0.5	Transportation expenses	0.5
Medical expenses	0.5	Medical expenses	0.5
Education expenses	0.5	Education expenses	0.5
Other expenses	0.5	Other expenses	0.5
Total expenses	0.5	Total expenses	0.5
Net income	0.5	Net income	0.5
Assets	0.5	Assets	0.5
Liabilities	0.5	Liabilities	0.5
Net worth	0.5	Net worth	0.5
Financial health	0.5	Financial health	0.5
Overall financial well-being	0.5	Overall financial well-being	0.5

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Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr Leu Arg Gly			
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Lys			
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Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala			
35	40	45	
Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Leu			
50	55	60	
Val Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala			
65	70	75	80
Arg Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala			
85	90	95	
Pro Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala			
100	105	110	
Glu Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys			
115	120	125	
Asn Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg			
130	135	140	
Lys Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly			
145	150	155	160
Arg Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile			
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Trp Leu Lys Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro			
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Lys Ile Tyr Leu Arg Gly Lys			
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 Val Ser Ser Ala Leu Lys Ser Ser Arg Ser Leu Ile Thr Pro Gln Val
 15 20 25

cct gcc tgc aca ggg ttt ttt ctt agt ttg ttg cct aag agt aca cca 146
 Pro Ala Cys Thr Gly Phe Phe Leu Ser Leu Leu Pro Lys Ser Thr Pro
 30 35 40

aat gtg aca tcc ttt cac caa tat aga tta ctt cat acc aca ttg tca 194
 Asn Val Thr Ser Phe His Gln Tyr Arg Leu Leu His Thr Thr Leu Ser
 45 50 55 60

agg aaa gga cta gaa gaa ttt ttt gat gac cca aaa aac tgg ggg caa 242
 Arg Lys Gly Leu Glu Glu Phe Phe Asp Asp Pro Lys Asn Trp Gly Gln
 65 70 75

gaa aaa gta aaa tct gga gca gca tgg acc tgt cag caa cta agg aac 290
 Glu Lys Val Lys Ser Gly Ala Ala Trp Thr Cys Gln Gln Leu Arg Asn
 80 85 90

aaa agt aat gaa gat tta cac aaa ctt tgg tat gtc tta ctg aaa gaa 338
 Lys Ser Asn Glu Asp Leu His Lys Leu Trp Tyr Val Leu Leu Lys Glu
 95 100 105

aga aac atg ctt cta acc cta gag cag gag gcc aag cgg cag aga ttg 386
 Arg Asn Met Leu Leu Thr Leu Glu Gln Glu Ala Lys Arg Gln Arg Leu
 110 115 120

cca atg cca agt cca gag cgg tta gat aag gta gta gat tcc atg gat 434
 Pro Met Pro Ser Pro Glu Arg Leu Asp Lys Val Val Asp Ser Met Asp
 125 130 135 140

gca tta gat aaa gtt gtc cag gaa aga gaa gat gcc cta agg ctt ctt 482
 Ala Leu Asp Lys Val Val Gln Glu Arg Glu Asp Ala Leu Arg Leu Leu
 145 150 155

cag act ggt caa gaa aga gct aga cct ggt gct tgg aga aga gac atc 530
 Gln Thr Gly Gln Glu Arg Ala Arg Pro Gly Ala Trp Arg Arg Asp Ile
 160 165 170

ttt gga aga atc atc tgg cac aag ttc aag cag tgg gtt ata cct tgg 578

09390688-092704

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Ile Trp His Lys Phe Lys Gln Trp Val Ile Pro Trp His Leu Asn Lys
180 185 190
Arg Tyr Asn Arg Lys Arg Phe Phe Ala Leu Pro Tyr Val Asp His Phe
195 200 205
Leu Arg Leu Glu Arg Glu Lys Arg Ala Arg Ile Lys Ala Arg Lys Glu
210 215 220
Asn Leu Glu Arg Lys Lys Ala Lys Ile Leu Leu Lys Lys Phe Pro His
225 230 235 240
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cggagtttgc t atg gac agc aac cat caa agt aat tac aaa ctc agt aaa 170
Met Asp Ser Asn His Gln Ser Asn Tyr Lys Leu Ser Lys
1 5 10

act gag aag aag ttc tta agg aaa cag att aaa gcc aag cat act ttg 218
Thr Glu Lys Lys Phe Leu Arg Lys Gln Ile Lys Ala Lys His Thr Leu
15 20 25

ctg aga cat gaa ggc att gag aca gta tcc tat gcc act cag agc ctg 266
Leu Arg His Glu Gly Ile Glu Thr Val Ser Tyr Ala Thr Gln Ser Leu
30 35 40 45

gtt gtt gcc aat ggt ggt ttg ggt aat ggt gtg agt cgg aac cag ctg 314
Val Val Ala Asn Gly Gly Leu Gly Asn Gly Val Ser Arg Asn Gln Leu
50 55 60

ctc ccg gtt tta gag aaa tgt gga ctg gtg gat gct ctc tta atg cca 362
Leu Pro Val Leu Glu Lys Cys Gly Leu Val Asp Ala Leu Leu Met Pro
65 70 75

cct aac aag ccg tac tca ttt gca aga tac aga act aca gaa gaa tct 410
Pro Asn Lys Pro Tyr Ser Phe Ala Arg Tyr Arg Thr Thr Glu Glu Ser
80 85 90

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Gly Gln Lys Ile Thr Leu Tyr Leu Asn Phe Val Glu Lys Val Gln Trp	
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aag gag ttg agg cct caa gcc tta cca cca gga ctc atg gta gta gaa	554
Lys Glu Leu Arg Pro Gln Ala Leu Pro Pro Gly Leu Met Val Val Glu	
130 135 140	
gaa ata att tct tct gag gag gag aaa atg ctt ttg gaa agt gtt gat	602
Glu Ile Ile Ser Ser Glu Glu Glu Lys Met Leu Leu Glu Ser Val Asp	
145 150 155	
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Trp Thr Glu Asp Thr Asp Asn Gln Asn Ser Gln Lys Ser Leu Lys His	
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aga aga gta aag cat ttt ggt tat gag ttc cac tat gag aac aac aat	698
Arg Arg Val Lys His Phe Gly Tyr Glu Phe His Tyr Glu Asn Asn Asn	
175 180 185	
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Val Asp Lys Asp Lys Pro Leu Ser Gly Gly Leu Pro Asp Ile Cys Glu	
190 195 200 205	
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Ser Phe Leu Glu Lys Trp Leu Arg Lys Gly Tyr Ile Lys His Lys Pro	
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Asp Gln Met Thr Ile Asn Gln Tyr Glu Pro Gly Gln Gly Ile Pro Ala	
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cat att gac aca cat tcc gct ttt gag gat gag atc gtt tct ctc agt	890
His Ile Asp Thr His Ser Ala Phe Glu Asp Glu Ile Val Ser Leu Ser	
240 245 250	
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Leu Gly Ser Glu Ile Val Met Asp Phe Lys His Pro Asp Gly Ile Ala	
255 260 265	
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Ser Arg Tyr Leu Trp Thr His Gly Ile Thr Cys Arg Lys Phe Asp Thr	
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Val Gln Ala Ser Glu Ser Leu Lys Ser Gly Ile Ile Thr Ser Asp Val	
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Gly Asp Leu Thr Leu Ser Lys Arg Gly Leu Arg Thr Ser Phe Thr Phe	
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Arg Lys Val Arg Gln Thr Pro Cys Asn Cys Ser Tyr Pro Leu Val Cys	
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Asp Ser Gln Arg Lys Glu Thr Pro Pro Ser Phe Pro Glu Ser Asp Lys	
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gaa gcc tca cgg ctg gag caa gag tac gtc cat cag gtt tat gaa gag	1274
Glu Ala Ser Arg Leu Glu Gln Glu Tyr Val His Gln Val Tyr Glu Glu	
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Ile Ala Gly His Phe Ser Ser Thr Arg His Thr Pro Trp Pro His Ile	
385 390 395	
gtg gag ttt ttg aag gct ttg cca agt ggt tca ata gtg gct gat att	1370
Val Glu Phe Leu Lys Ala Leu Pro Ser Gly Ser Ile Val Ala Asp Ile	
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Gly Cys Gly Asn Gly Lys Tyr Leu Gly Ile Asn Lys Glu Leu Tyr Met	
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gag cgt aga gtg gca gct ctc caa gaa att gtt cga ctc ctg aga cca	1466
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Gly Gly Lys Ala Leu Ile Tyr Val Trp Ala Met Glu Gln Glu Tyr Asn	
450 455 460	
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Lys Gln Lys Ser Lys Tyr Leu Arg Gly Asn Arg Asn Ser Gln Gly Lys	
465 470 475	
aaa gag gag atg aac agt gat acc tca gtg cag agg tca ctt gtg gag	1610
Lys Glu Glu Met Asn Ser Asp Thr Ser Val Gln Arg Ser Leu Val Glu	
480 485 490	
caa atg cgt gac atg ggc agt cga gac tcg gca tct tct gtc ccc cgc	1658
Gln Met Arg Asp Met Gly Ser Arg Asp Ser Ala Ser Ser Val Pro Arg	
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Ile Asn Asp Ser Gln Glu Gly Gly Cys Asn Ser Arg Gln Val Ser Asn	
510 515 520 525	
tcc aag ctg cct gtt cat gtt aac agg act tct ttt tat tct caa gat	1754
Ser Lys Leu Pro Val His Val Asn Arg Thr Ser Phe Tyr Ser Gln Asp	
530 535 540	
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His	Arg	Tyr	Tyr	His	Val	Phe	Arg	Glu	Gly	Glu	Leu	Glu	Gly	Ala	Cys		
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Asn	Trp	Cys	Val	Ile	Leu	Gln	Lys	Ala									
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35 40 45
Asn Gly Gly Leu Gly Asn Gly Val Ser Arg Asn Gln Leu Leu Pro Val
50 55 60
Leu Glu Lys Cys Gly Leu Val Asp Ala Leu Leu Met Pro Pro Asn Lys
65 70 75 80
Pro Tyr Ser Phe Ala Arg Tyr Arg Thr Thr Glu Glu Ser Lys Arg Ala
85 90 95
Tyr Val Thr Leu Asn Gly Lys Glu Val Val Asp Asp Leu Gly Gln Lys
100 105 110
Ile Thr Leu Tyr Leu Asn Phe Val Glu Lys Val Gln Trp Lys Glu Leu
115 120 125

Arg Pro Gln Ala Leu Pro Pro Gly Leu Met Val Val Glu Glu Ile Ile
130 135 140

Ser Ser Glu Glu Glu Lys Met Leu Leu Glu Ser Val Asp Trp Thr Glu
145 150 155 160

Asp Thr Asp Asn Gln Asn Ser Gln Lys Ser Leu Lys His Arg Arg Val
165 170 175

Lys His Phe Gly Tyr Glu Phe His Tyr Glu Asn Asn Asn Val Asp Lys
180 185 190

Asp Lys Pro Leu Ser Gly Gly Leu Pro Asp Ile Cys Glu Ser Phe Leu
195 200 205

Glu Lys Trp Leu Arg Lys Gly Tyr Ile Lys His Lys Pro Asp Gln Met
210 215 220

Thr Ile Asn Gln Tyr Glu Pro Gly Gln Gly Ile Pro Ala His Ile Asp
225 230 235 240

Thr His Ser Ala Phe Glu Asp Glu Ile Val Ser Leu Ser Leu Gly Ser
245 250 255

Glu Ile Val Met Asp Phe Lys His Pro Asp Gly Ile Ala Val Pro Val
260 265 270

Met Leu Pro Arg Arg Ser Leu Leu Val Met Thr Gly Glu Ser Arg Tyr
275 280 285

Leu Trp Thr His Gly Ile Thr Cys Arg Lys Phe Asp Thr Val Gln Ala
290 295 300

Ser Glu Ser Leu Lys Ser Gly Ile Ile Thr Ser Asp Val Gly Asp Leu
305 310 315 320

Thr Leu Ser Lys Arg Gly Leu Arg Thr Ser Phe Thr Phe Arg Lys Val
325 330 335

Arg Gln Thr Pro Cys Asn Cys Ser Tyr Pro Leu Val Cys Asp Ser Gln
340 345 350

Arg Lys Glu Thr Pro Pro Ser Phe Pro Glu Ser Asp Lys Glu Ala Ser
355 360 365

Arg Leu Glu Gln Glu Tyr Val His Gln Val Tyr Glu Glu Ile Ala Gly
370 375 380

His Phe Ser Ser Thr Arg His Thr Pro Trp Pro His Ile Val Glu Phe
385 390 395 400

Leu Lys Ala Leu Pro Ser Gly Ser Ile Val Ala Asp Ile Gly Cys Gly
405 410 415

Asn Gly Lys Tyr Leu Gly Ile Asn Lys Glu Leu Tyr Met Glu Arg Arg
420 425 430

25	30	35	
aag gag ctg ctg gga cag ggg att gat tat gag aag atc ctg aag ctc Lys Glu Leu Leu Gly Gln Gly Ile Asp Tyr Glu Lys Ile Leu Lys Leu 40 45 50			197
acg gct gac gcc aag ttt gag tca ggc gat gtg aag gcc aca gtg gca Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp Val Lys Ala Thr Val Ala 55 60 65 70			245
gtg ctg agt ttc atc ctc tcc agt gcg gcc aag cac agt gtc gat ggc Val Leu Ser Phe Ile Leu Ser Ser Ala Ala Lys His Ser Val Asp Gly 75 80 85			293
gaa tcc ttg tcc agt gaa ctg cag cag ctg ggg ctg ccc aaa gag cac Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu Gly Leu Pro Lys Glu His 90 95 100			341
gcg gcc agc ctg tgc cgc tgt tat gag gag aag caa agc ccc ttg cag Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu Lys Gln Ser Pro Leu Gln 105 110 115			389
aag cac ttg cgg gtc tgc agc cta cgc atg aat agg ttg gca ggt gtg Lys His Leu Arg Val Cys Ser Leu Arg Met Asn Arg Leu Ala Gly Val 120 125 130			437
ggc tgg cgg gtg gac tac acc ctg agc tcc agc ctg ctg caa tcc gtg Gly Trp Arg Val Asp Tyr Thr Leu Ser Ser Ser Leu Leu Gln Ser Val 135 140 145 150			485
gaa gag ccc atg gtg cac ctg cgg ctg gag gtg gca gct gcc cca ggg Glu Glu Pro Met Val His Leu Arg Leu Glu Val Ala Ala Ala Pro Gly 155 160 165			533
acc cca gcc cag cct gtt gcc atg tcc ctc tca gca gac aag ttc cag Thr Pro Ala Gln Pro Val Ala Met Ser Leu Ser Ala Asp Lys Phe Gln 170 175 180			581
gtc ctc ctg gca gaa ctg aag cag gcc cag acc ctg atg agc tcc ctg Val Leu Leu Ala Glu Leu Lys Gln Ala Gln Thr Leu Met Ser Ser Leu 185 190 195			629
ggc tga ggagaagggg gttccaggcc tgtgtggagc cgccctgccc gtatggagtc Gly			685
acgccctctg aactgctctt cgggaggcag ccctgggttct aggatgctga ggccctggcc			745
cggactctgg cctcccagat cccagctgc ctcaattctc tcttgagaac ttggctcagg			805
gctcctgagg acctttccca gcattacctt cccttccctt gaaaggcaat tggttgctgt			865
tttcataagc aggaaaaata aacagaagta taaagg			901

<210> 20
<211> 199
<212> PRT

<213> Homo sapiens

<400> 20

Met Arg Phe Arg Phe Cys Gly Asp Leu Asp Cys Pro Asp Trp Val Leu
1 5 10 15

Ala Glu Ile Ser Thr Leu Ala Lys Met Ser Ser Val Lys Leu Arg Leu
20 25 30

Leu Cys Ser Gln Val Leu Lys Glu Leu Leu Gly Gln Gly Ile Asp Tyr
35 40 45

Glu Lys Ile Leu Lys Leu Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp
50 55 60

Val Lys Ala Thr Val Ala Val Leu Ser Phe Ile Leu Ser Ser Ala Ala
65 70 75 80

Lys His Ser Val Asp Gly Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu
85 90 95

Gly Leu Pro Lys Glu His Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu
100 105 110

Lys Gln Ser Pro Leu Gln Lys His Leu Arg Val Cys Ser Leu Arg Met
115 120 125

Asn Arg Leu Ala Gly Val Gly Trp Arg Val Asp Tyr Thr Leu Ser Ser
130 135 140

Ser Leu Leu Gln Ser Val Glu Glu Pro Met Val His Leu Arg Leu Glu
145 150 155 160

Val Ala Ala Ala Pro Gly Thr Pro Ala Gln Pro Val Ala Met Ser Leu
165 170 175

Ser Ala Asp Lys Phe Gln Val Leu Leu Ala Glu Leu Lys Gln Ala Gln
180 185 190

Thr Leu Met Ser Ser Leu Gly
195

<210> 21

<211> 1274

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (131)..(1111)

<400> 21

acagcgcgctc gcggcagccc ccaaggaaga ccagcctgcc tctggctcgt tcttggcgct 60

ctgcgttttcg tgaccttgct cagtagaagg ctatttaatt ttcacaactg cttgaatttt 120

gacatacaag atg aag caa gat gcc tca aga aat gct gcc tac act gtg	169
Met Lys Gln Asp Ala Ser Arg Asn Ala Ala Tyr Thr Val	
1 5 10	
gat tgt gaa gat tat gtg cat gtg gta gaa ttt aat ccc ttt gag aat	217
Asp Cys Glu Asp Tyr Val His Val Val Glu Phe Asn Pro Phe Glu Asn	
15 20 25	
ggg gat tca gga aac cta att gca tat ggt ggc aat aat tat gtg gtc	265
Gly Asp Ser Gly Asn Leu Ile Ala Tyr Gly Gly Asn Asn Tyr Val Val	
30 35 40 45	
att ggc acg tgt acg ttt cag gaa gaa gaa gca gac gtt gaa ggc att	313
Ile Gly Thr Cys Thr Phe Gln Glu Glu Ala Asp Val Glu Gly Ile	
50 55 60	
cag tat aaa aca ctt cga aca ttt cac cat gga gtc agg gtt gat ggc	361
Gln Tyr Lys Thr Leu Arg Thr Phe His His Gly Val Arg Val Asp Gly	
65 70 75	
ata gct tgg agc cca gag act aga ctt gat tca ttg cct cca gta atc	409
Ile Ala Trp Ser Pro Glu Thr Arg Leu Asp Ser Leu Pro Pro Val Ile	
80 85 90	
aaa ttt tgt act tca gct gct gat atg aaa att aga tta ttt act tca	457
Lys Phe Cys Thr Ser Ala Ala Asp Met Lys Ile Arg Leu Phe Thr Ser	
95 100 105	
gat ctt cag gat aaa aat gaa tat aag gtt tta gag ggc cat acc gat	505
Asp Leu Gln Asp Lys Asn Glu Tyr Lys Val Leu Glu Gly His Thr Asp	
110 115 120 125	
ttc att aat ggt ttg gtg ttt gat ccc aaa gaa ggc caa gaa att gca	553
Phe Ile Asn Gly Leu Val Phe Asp Pro Lys Glu Gly Gln Glu Ile Ala	
130 135 140	
agt gtg agt gac gat cac acc tgc agg att tgg aac ttg gaa gga gtg	601
Ser Val Ser Asp Asp His Thr Cys Arg Ile Trp Asn Leu Glu Gly Val	
145 150 155	
caa aca gct cat ttt gtt ctt cat tct cct ggc atg agt gtg tgc tgg	649
Gln Thr Ala His Phe Val Leu His Ser Pro Gly Met Ser Val Cys Trp	
160 165 170	
cat cct gag gag act ttt aag cta atg gtt gca gag aag aat gga aca	697
His Pro Glu Glu Thr Phe Lys Leu Met Val Ala Glu Lys Asn Gly Thr	
175 180 185	
atc cgg ttt tat gat ctt ttg gcc caa cag gct att tta tct ctt gaa	745
Ile Arg Phe Tyr Asp Leu Leu Ala Gln Gln Ala Ile Leu Ser Leu Glu	
190 195 200 205	
tca gaa caa gtg cca tta atg tca gca cac tgg tgc tta aaa aac acc	793
Ser Glu Gln Val Pro Leu Met Ser Ala His Trp Cys Leu Lys Asn Thr	
210 215 220	
ttc aaa gtt gga gcc gtt gca gga aat gat tgg tta att tgg gat att	841

Phe Lys Val Gly Ala Val Ala Gly Asn Asp Trp Leu Ile Trp Asp Ile
225 230 235

act cgg tcc agt tat cct caa aat aag aga cct gtt cac atg gat cga 889
Thr Arg Ser Ser Tyr Pro Gln Asn Lys Arg Pro Val His Met Asp Arg
240 245 250

gcc tgc tta ttc agg tgg tcc aca att agt gaa aat ctg ttt gca acc 937
Ala Cys Leu Phe Arg Trp Ser Thr Ile Ser Glu Asn Leu Phe Ala Thr
255 260 265

act ggt tat cct ggc aaa atg gca agc cag ttt caa att cat cat tta 985
Thr Gly Tyr Pro Gly Lys Met Ala Ser Gln Phe Gln Ile His His Leu
270 275 280 285

gga cac cct cag ccc atc ctc atg ggt tct gta gcc gtt gga tct gga 1033
Gly His Pro Gln Pro Ile Leu Met Gly Ser Val Ala Val Gly Ser Gly
290 295 300

ctg tcc tgg cat cga act ctc cct ctg tgt gta att gga gga gac cac 1081
Leu Ser Trp His Arg Thr Leu Pro Leu Cys Val Ile Gly Gly Asp His
305 310 315

aag ctg ttg ttt tgg gtg act gaa gta taa agtgttttct gtaccttaga 1131
Lys Leu Leu Phe Trp Val Thr Glu Val
320 325

ttcacaaact ttgtatTTTT agtacatatt ttgaagaatt tctatagtagc atatttttgaa 1191

gaatttttat atcaaatata ccgtatactt tagaaaatgt ctcagttgct tttatttaa 1251

aaaatgttga tggtttgaaa aat 1274

<210> 22

<211> 326

<212> PRT

<213> Homo sapiens

<400> 22

Met Lys Gln Asp Ala Ser Arg Asn Ala Ala Tyr Thr Val Asp Cys Glu
1 5 10 15

Asp Tyr Val His Val Val Glu Phe Asn Pro Phe Glu Asn Gly Asp Ser
20 25 30

Gly Asn Leu Ile Ala Tyr Gly Gly Asn Asn Tyr Val Val Ile Gly Thr
35 40 45

Cys Thr Phe Gln Glu Glu Glu Ala Asp Val Glu Gly Ile Gln Tyr Lys
50 55 60

Thr Leu Arg Thr Phe His His Gly Val Arg Val Asp Gly Ile Ala Trp
65 70 75 80

Ser Pro Glu Thr Arg Leu Asp Ser Leu Pro Pro Val Ile Lys Phe Cys
85 90 95

cttttcgagg taggagtcga ctctgtgag gt atg gtg ctg ggt gca gat gca 53
Met Val Leu Gly Ala Asp Ala
1 5

gtg tgg ctc tgg ata gca cct tat gga cag ttg tgt ccc caa gga agg 101
Val Trp Leu Trp Ile Ala Pro Tyr Gly Gln Leu Cys Pro Gln Gly Arg
10 15 20

atg aga ata gct act gaa gtc cta aag agc aag cct aac tca agc cat 149
Met Arg Ile Ala Thr Glu Val Leu Lys Ser Lys Pro Asn Ser Ser His
25 30 35

tgg cac aca ggc att aga cag aaa gct gga agt tga aatggtggag 195
Trp His Thr Gly Ile Arg Gln Lys Ala Gly Ser
40 45 50

tccaacttgc ctggaccagc ttaatgggtc tgctcctggt aacgttttta tccatggatg 255

acttgcttgg gtaaggacat gaagacagtt cctgtcatac cttttaaagg tacatgtttt 315

attgatgtta acgttaattg attgagctac tgtagtgat gatttttaaaa ttaaagcaga 375

tgggaatctc tctgagaaag aaaatggaga ttaatcttaa actgaaacag tagttgggaa 435

atctttttaga aatccaccta ttactaccta ttggtaaagg agattaaatt tctacaggta 495

tggagagtcg gcttgactac actgtgtgga gcaagtttta aagaagcaaa ggactcagaa 555

ttcatgattg aagaaatgca ggcagacctg ttatcctaaa ctaggtgagt cagcttttgg 615

tacatgtgat gattttcagt gtaaccaatg atgtaatgat tctgccaaat gaaatataat 675

gatatcactg taaaaccgtt ccattttgat tctgaggtta ctctactaac aagcatcaca 735

catttgattt ttgccctgat taatatgttg gcttcgcttt cagggttttt aatgaccaca 795

acaagcaagc atgcagctta ctgcttgaaa gggctcttgcc tcacccaagc tagagtgcag 855

tggcctttga agcttactac agcctcaaac ttctgggctc aagtgatcct cagcctccca 915

gtggctcttg tagactgcct gatggagtct catggcacia gaagattaaa acagtgtctc 975

caattttaat aaatttttgc aatcc 1000

<210> 24
<211> 50
<212> PRT
<213> Homo sapiens

<400> 24
Met Val Leu Gly Ala Asp Ala Val Trp Leu Trp Ile Ala Pro Tyr Gly
1 5 10 15
Gln Leu Cys Pro Gln Gly Arg Met Arg Ile Ala Thr Glu Val Leu Lys
20 25 30

Ser Lys Pro Asn Ser Ser His Trp His Thr Gly Ile Arg Gln Lys Ala
 35 40 45

Gly Ser
 50

<210> 25
 <211> 1087
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (28)..(558)

<400> 25
 agcttccggg tttcctgggc tactacg atg gcg atg agt ttc gag tgg ccg tgg 54
 Met Ala Met Ser Phe Glu Trp Pro Trp
 1 5

cag tat cgc ttc cca ccc ttc ttt acg tta caa ccg aat gtg gac act 102
 Gln Tyr Arg Phe Pro Pro Phe Phe Thr Leu Gln Pro Asn Val Asp Thr
 10 15 20 25

cgg cag aag cag ctg gcc gcc tgg tgc tcg ctg gtc ctg tcc ttc tgc 150
 Arg Gln Lys Gln Leu Ala Ala Trp Cys Ser Leu Val Leu Ser Phe Cys
 30 35 40

cgc ctg cac aaa cag tcc agc atg acg gtg atg gaa gct cag gag agc 198
 Arg Leu His Lys Gln Ser Ser Met Thr Val Met Glu Ala Gln Glu Ser
 45 50 55

ccg ctc ttc aac aac gtc aag cta cag cga aag ctt cct gtg gag tcg 246
 Pro Leu Phe Asn Asn Val Lys Leu Gln Arg Lys Leu Pro Val Glu Ser
 60 65 70

atc cag att gta tta gag gaa ctg agg aag aaa ggg aac ctc gag tgg 294
 Ile Gln Ile Val Leu Glu Glu Leu Arg Lys Lys Gly Asn Leu Glu Trp
 75 80 85

ttg gat aag agc aag tcc agc ttc ctg atc atg tgg cgg agg cca gaa 342
 Leu Asp Lys Ser Lys Ser Ser Phe Leu Ile Met Trp Arg Arg Pro Glu
 90 95 100 105

gaa tgg ggg aaa ctc atc tat cag tgg gtt tcc agg agt ggc cag aac 390
 Glu Trp Gly Lys Leu Ile Tyr Gln Trp Val Ser Arg Ser Gly Gln Asn
 110 115 120

aac tcc gtc ttt acc ctg tat gaa ctg act aat ggg gaa gac aca gag 438
 Asn Ser Val Phe Thr Leu Tyr Glu Leu Thr Asn Gly Glu Asp Thr Glu
 125 130 135

gat gag gag ttc cac ggg ctg gat gaa gcc act cta ctg cgg gct ctg 486
 Asp Glu Glu Phe His Gly Leu Asp Glu Ala Thr Leu Leu Arg Ala Leu
 140 145 150

09690633.092701

cag gcc cta cag cag gag cac aag gcc gag atc atc act gtc agc gat 534
 Gln Ala Leu Gln Gln Glu His Lys Ala Glu Ile Ile Thr Val Ser Asp
 155 160 165

ggc cga ggc gtc aag ttc ttc tag cagggacctg tctcccttta cttcttacct 588
 Gly Arg Gly Val Lys Phe Phe
 170 175

cccacctttc cagggctttc aaaaggagac agaccacagtg tcccccaaag actggatctg 648
 tgactccacc agactcaaaa ggactccagt cctgaaggct gggacctggg gatgggtttc 708
 tcacacccca tatgtctgtc ccttggatag ggtgaggctg aagcaccagg gagaaaatat 768
 gtgcttcttc tcgccctacc tcctttccca tcctagactg tccttgagcc aggggtctgta 828
 aacctgacac tttatatgtg ttcacacatg taagtacata cacacatgcg cctgcagcac 888
 atgcttctgt ctctctctcc tcccaccct ttagctgctg ttgcctccct tctcaggctg 948
 gtgctggatc cttcctaggg gatgggggaa gccttgctg caggcagcct tccaggcaat 1008
 atgaagatag gaggccacg ggcttggcag tgagaggtgt ggccccacac cgatttatga 1068
 tattaaaatc tcaactccc 1087

<210> 26
 <211> 176
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Ala Met Ser Phe Glu Trp Pro Trp Gln Tyr Arg Phe Pro Pro Phe
 1 5 10 15
 Phe Thr Leu Gln Pro Asn Val Asp Thr Arg Gln Lys Gln Leu Ala Ala
 20 25 30
 Trp Cys Ser Leu Val Leu Ser Phe Cys Arg Leu His Lys Gln Ser Ser
 35 40 45
 Met Thr Val Met Glu Ala Gln Glu Ser Pro Leu Phe Asn Asn Val Lys
 50 55 60
 Leu Gln Arg Lys Leu Pro Val Glu Ser Ile Gln Ile Val Leu Glu Glu
 65 70 75 80
 Leu Arg Lys Lys Gly Asn Leu Glu Trp Leu Asp Lys Ser Lys Ser Ser
 85 90 95
 Phe Leu Ile Met Trp Arg Arg Pro Glu Glu Trp Gly Lys Leu Ile Tyr
 100 105 110
 Gln Trp Val Ser Arg Ser Gly Gln Asn Asn Ser Val Phe Thr Leu Tyr
 115 120 125

Glu Leu Thr Asn Gly Glu Asp Thr Glu Asp Glu Glu Phe His Gly Leu
 130 135 140

Asp Glu Ala Thr Leu Leu Arg Ala Leu Gln Ala Leu Gln Gln Glu His
 145 150 155 160

Lys Ala Glu Ile Ile Thr Val Ser Asp Gly Arg Gly Val Lys Phe Phe
 165 170 175

<210> 27
 <211> 703
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (67)..(222)

<400> 27
 cgggcgcgag gcggccaccg tggagagcag agcgcgggcgg ctggaagctg ctaagtcaga 60

gccgcg atg ttc cgg att gag ggc ctc gcg ccg aag ctg gac ccg gag 108
 Met Phe Arg Ile Glu Gly Leu Ala Pro Lys Leu Asp Pro Glu
 1 5 10

gag atg aaa cgg aag atg cgc gag gat gtg atc tcc tcc ata cgg aac 156
 Glu Met Lys Arg Lys Met Arg Glu Asp Val Ile Ser Ser Ile Arg Asn
 15 20 25 30

ttt ctc atc tac gtg gcc ctc ctg cga gtc act cca ttt atc tta aag 204
 Phe Leu Ile Tyr Val Ala Leu Leu Arg Val Thr Pro Phe Ile Leu Lys
 35 40 45

aaa ttg gac agc ata tga agacaggaca tcacatatga atgcacgata 252
 Lys Leu Asp Ser Ile
 50

tgaagagcct ggttacagtt tcgactcctc tctgcaagtg aataggccca gaaaggtgta 312

agagactcct tgaatggaca taaaattctg cttgttaaga acaagtttgg ctctggtaac 372

tgaccttcaa agctaaaata taaaactatt tgggaagtat gaaacgatgt ctcgtgatct 432

ggtgtaccct tatccctgtg acgtttggcc cctgacaata ctggtataat tgtaaataat 492

gtcaaactcc gttttctagc aagtattaag ggagctgtgt ctgaaatggc actgtcttgt 552

cagtcatttc tgtttacctt tttcttctgc ccagagtgtg tttgtgaaga gtctcttata 612

ttatgttttg tggaaatcag cacacaacca caatgacatt taagcacagg atcattatta 672

gtctatgttt ttaataaaca tatcaattaa g 703

<210> 28
 <211> 51

<212> PRT
<213> Homo sapiens

<400> 28

Met Phe Arg Ile Glu Gly Leu Ala Pro Lys Leu Asp Pro Glu Glu Met
1 5 10 15
Lys Arg Lys Met Arg Glu Asp Val Ile Ser Ser Ile Arg Asn Phe Leu
20 25 30
Ile Tyr Val Ala Leu Leu Arg Val Thr Pro Phe Ile Leu Lys Lys Leu
35 40 45
Asp Ser Ile
50

<210> 29

<211> 921

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (204)..(776)

<400> 29

ctcccccggc gcggtccgcc aggccagtgc cctcagcatc tccaccccga ggtgggtttga 60
actttgagcc ttttgtagtc ctgatgaata atttcatttt cctcaagttt atgacactcg 120
gaacgtcaag aactggaggt ttgtgcaatt tgagaccggt cggcactgtg cagagatcag 180
agtactaaga gacagagatt aaa atg gct tcc aga gga aag aca gag aca agc 233
Met Ala Ser Arg Gly Lys Thr Glu Thr Ser
1 5 10
aaa tta aag cag aat tta gaa gaa cag ttg gat aga ctc atg caa caa 281
Lys Leu Lys Gln Asn Leu Glu Glu Gln Leu Asp Arg Leu Met Gln Gln
15 20 25
tta caa gat ctg gag gaa tgc aga gag gaa ctt gat aca gat gaa tat 329
Leu Gln Asp Leu Glu Glu Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr
30 35 40
gaa gaa acc aaa aag gaa act ctg gag caa cta agt gaa ttt aat gat 377
Glu Glu Thr Lys Lys Glu Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp
45 50 55
tca cta aag aaa att atg tct gga aat atg act ttg gta gat gaa cta 425
Ser Leu Lys Lys Ile Met Ser Gly Asn Met Thr Leu Val Asp Glu Leu
60 65 70
agt gga atg cag ctg gct att cag gca gct atc agc cag gcc ttt aaa 473
Ser Gly Met Gln Leu Ala Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys
75 80 85 90

09090600 09090600

acc cca gag gtc atc aga ttg ttt gca aag aaa caa cca ggt cag ctt 521
 Thr Pro Glu Val Ile Arg Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu
 95 100 105

cgg aca agg tta gca gag atg gat aga gat ctg atg gta gga aag ctg 569
 Arg Thr Arg Leu Ala Glu Met Asp Arg Asp Leu Met Val Gly Lys Leu
 110 115 120

gaa aga gac ctg tac act caa cag aaa gtg gag ata cta aca gct ctt 617
 Glu Arg Asp Leu Tyr Thr Gln Gln Lys Val Glu Ile Leu Thr Ala Leu
 125 130 135

agg aaa ctt gga gag aag ctg act gca gat gat gag gcc ttc ttg tca 665
 Arg Lys Leu Gly Glu Lys Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser
 140 145 150

gca aat gca ggt gct ata ctc agc cag ttt gag aaa gtc tct aca gac 713
 Ala Asn Ala Gly Ala Ile Leu Ser Gln Phe Glu Lys Val Ser Thr Asp
 155 160 165 170

ctt ggc tct gga gac aaa att ctt gct ctg gca agt ttt gag gtt gaa 761
 Leu Gly Ser Gly Asp Lys Ile Leu Ala Leu Ala Ser Phe Glu Val Glu
 175 180 185

aaa aca aaa aaa tga catggtgcag aagcttgtaa cattgatcac attcttaatg 816
 Lys Thr Lys Lys
 190

taaatggtgt ctttcttctg gggttttcag ttattgcaaaa gaaatgaaga gattctggaa 876

atgcatcaat aacctaagaa aaagcgacat aaaaatatac ttatg 921

<210> 30
 <211> 190
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Ala Ser Arg Gly Lys Thr Glu Thr Ser Lys Leu Lys Gln Asn Leu
 1 5 10 15

Glu Glu Gln Leu Asp Arg Leu Met Gln Gln Leu Gln Asp Leu Glu Glu
 20 25 30

Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr Glu Glu Thr Lys Lys Glu
 35 40 45

Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp Ser Leu Lys Lys Ile Met
 50 55 60

Ser Gly Asn Met Thr Leu Val Asp Glu Leu Ser Gly Met Gln Leu Ala
 65 70 75 80

Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys Thr Pro Glu Val Ile Arg
 85 90 95

Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu Arg Thr Arg Leu Ala Glu
100 105 110

Met Asp Arg Asp Leu Met Val Gly Lys Leu Glu Arg Asp Leu Tyr Thr
115 120 125

Gln Gln Lys Val Glu Ile Leu Thr Ala Leu Arg Lys Leu Gly Glu Lys
130 135 140

Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser Ala Asn Ala Gly Ala Ile
145 150 155 160

Leu Ser Gln Phe Glu Lys Val Ser Thr Asp Leu Gly Ser Gly Asp Lys
165 170 175

Ile Leu Ala Leu Ala Ser Phe Glu Val Glu Lys Thr Lys Lys
180 185 190

<210> 31
<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (41)..(418)

<400> 31
ttttttccgg ttccggcctg gcgagagttt gtgcggcgac atg aaa ctg ctt acc 55
Met Lys Leu Leu Thr
1 5

cac aat ctg ctg agc tcg cat gtg cgg ggg gtg ggg tcc cgt ggc ttc 103
His Asn Leu Leu Ser Ser His Val Arg Gly Val Gly Ser Arg Gly Phe
10 15 20

ccc ctg cgc ctc cag gcc acc gag gtc cgt atc tgc cct gtg gaa ttc 151
Pro Leu Arg Leu Gln Ala Thr Glu Val Arg Ile Cys Pro Val Glu Phe
25 30 35

aac ccc aac ttc gtg gcg cgt atg ata cct aaa gtg gag tgg tcg gcg 199
Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys Val Glu Trp Ser Ala
40 45 50

ttc ctg gag gcg gcc gat aac ttg cgt ctg atc cag gtg ccg aaa ggg 247
Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile Gln Val Pro Lys Gly
55 60 65

ccg gtt gag gga tat gag gag aat gag gag ttt ctg agg acc atg cac 295
Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe Leu Arg Thr Met His
70 75 80 85

cac ctg ctg ctg gag gtg gaa gtg ata gag ggc acc ctg cag tgc ccg 343
His Leu Leu Leu Glu Val Glu Val Ile Glu Gly Thr Leu Gln Cys Pro
90 95 100

Met Ala Ala Arg Gly Arg Arg Ala Glu															
1								5							
cct cag ggc cgg gag gct ccg ggc ccc gcg ggc ggt ggc ggt ggc ggg	99														
Pro Gln Gly Arg Glu Ala Pro Gly Pro Ala Gly Gly Gly Gly Gly Gly															
10 15 20 25															
agc cgt tgg gct gag tcg gga tcg ggg acg tcg ccc gag agc ggg gac	147														
Ser Arg Trp Ala Glu Ser Gly Ser Gly Thr Ser Pro Glu Ser Gly Asp															
30 35 40															
gag gag gtg tcg ggc gcg ggt tcg agc ccg gtg tcg ggc ggc gtg aac	195														
Glu Glu Val Ser Gly Ala Gly Ser Ser Pro Val Ser Gly Gly Val Asn															
45 50 55															
ttg ttc gcc aac gac ggc agc ttc ctg gag ctg ttc aag cgg aag atg	243														
Leu Phe Ala Asn Asp Gly Ser Phe Leu Glu Leu Phe Lys Arg Lys Met															
60 65 70															
gag gag gag cag cgg cag cgg cag gag gag ccg ccc ccg ggt ccg cag	291														
Glu Glu Glu Gln Arg Gln Arg Gln Glu Glu Pro Pro Pro Gly Pro Gln															
75 80 85															
cga ccc gac cag tcg gcc gcc gcc gct ggc ccc ggg gat ccg aag agg	339														
Arg Pro Asp Gln Ser Ala Ala Ala Ala Gly Pro Gly Asp Pro Lys Arg															
90 95 100 105															
aag ggc ggt ccg ggc tcc aca ctt agc ttc gtg ggc aaa cgc aga ggc	387														
Lys Gly Gly Pro Gly Ser Thr Leu Ser Phe Val Gly Lys Arg Arg Gly															
110 115 120															
ggg aac aaa cta gcc ctc aag acg gga ata gta gcc aag aag cag aag	435														
Gly Asn Lys Leu Ala Leu Lys Thr Gly Ile Val Ala Lys Lys Gln Lys															
125 130 135															
acg gag gat gag gta tta aca agt aaa ggt gac gcg tgg gcc aag tac	483														
Thr Glu Asp Glu Val Leu Thr Ser Lys Gly Asp Ala Trp Ala Lys Tyr															
140 145 150															
atg gca gaa gtg aaa aag tac aaa gct cac cag tgc ggt gac gat gat	531														
Met Ala Glu Val Lys Lys Tyr Lys Ala His Gln Cys Gly Asp Asp Asp															
155 160 165															
aaa act cgg ccc ctg gtg aaa tga cgccccctccc ccacctgccc atggcctggg	585														
Lys Thr Arg Pro Leu Val Lys															
170 175															
actctctgcg atgtacataa ctatttaatg cagcggcagc ggcgacagcc ttccctgaga	645														
ggacttaaaa gcagaaggaa accgagatgc ttcccgagc cgtggacgat tctccaggac	705														
tcttttttta ccttgagcac ttgcctcgtg agacttcata gaacagtggg ttactgtccc	765														
cccccttctca cctcctcatt ctctctgggt ctttctgtct tctctctctc accctcctcc	825														
ctcccccttag ccatcacttc tgggaagtaa agaacttgac ttagtgccgg	875														

<210> 34
 <211> 176
 <212> PRT
 <213> Homo sapiens

<400> 34
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 Gly Pro Ala Gly Gly Gly Gly Gly Gly Ser Arg Trp Ala Glu Ser Gly
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 Ser Gly Thr Ser Pro Glu Ser Gly Asp Glu Glu Val Ser Gly Ala Gly
 35 40 45
 Ser Ser Pro Val Ser Gly Gly Val Asn Leu Phe Ala Asn Asp Gly Ser
 50 55 60
 Phe Leu Glu Leu Phe Lys Arg Lys Met Glu Glu Glu Gln Arg Gln Arg
 65 70 75 80
 Gln Glu Glu Pro Pro Pro Gly Pro Gln Arg Pro Asp Gln Ser Ala Ala
 85 90 95
 Ala Ala Gly Pro Gly Asp Pro Lys Arg Lys Gly Gly Pro Gly Ser Thr
 100 105 110
 Leu Ser Phe Val Gly Lys Arg Arg Gly Gly Asn Lys Leu Ala Leu Lys
 115 120 125
 Thr Gly Ile Val Ala Lys Lys Gln Lys Thr Glu Asp Glu Val Leu Thr
 130 135 140
 Ser Lys Gly Asp Ala Trp Ala Lys Tyr Met Ala Glu Val Lys Lys Tyr
 145 150 155 160
 Lys Ala His Gln Cys Gly Asp Asp Asp Lys Thr Arg Pro Leu Val Lys
 165 170 175

<210> 35
 <211> 470
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (216)..(374)

<400> 35
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 tttaagtttc aaattgacat tccagacaag cgggtgcctga gcccgctgcct gtcttcagat 120
 cttcacagca cagttcctgg gaaggtggag ccaccagcct ctcttgaat aactgggaga 180

1042250"09906960

tgaacagga agctctatga cacacttgat cgaat atg aca gac acc gaa aat 233
Met Thr Asp Thr Glu Asn
1 5

cac gac tca gcc ccc tcc agc acc tct acc tgt tgc ccg ccg atc aca 281
His Asp Ser Ala Pro Ser Ser Thr Ser Thr Cys Cys Pro Pro Ile Thr
10 15 20

gcc gga atg cag ctg aaa gat tcc ctg ggg cct ggt tcc aac cgc cca 329
Ala Gly Met Gln Leu Lys Asp Ser Leu Gly Pro Gly Ser Asn Arg Pro
25 30 35

ctg tgg act ctg agg cct ctg cat ttg tgg gtg gtc tgc ctg tga 374
Leu Trp Thr Leu Arg Pro Leu His Leu Trp Val Val Cys Leu
40 45 50

tattttggtc atgggctggt ctggctgggt tcccatttgt ctggccagtc tctatgtgtc 434

ttaatccctt gtccttcatt aaaagcaaaa cttaaag 470

<210> 36
<211> 52
<212> PRT
<213> Homo sapiens

<400> 36
Met Thr Asp Thr Glu Asn His Asp Ser Ala Pro Ser Ser Thr Ser Thr
1 5 10 15

Cys Cys Pro Pro Ile Thr Ala Gly Met Gln Leu Lys Asp Ser Leu Gly
20 25 30

Pro Gly Ser Asn Arg Pro Leu Trp Thr Leu Arg Pro Leu His Leu Trp
35 40 45

Val Val Cys Leu
50

<210> 37
<211> 2920
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (73)..(2652)

<400> 37
aggtagcgc gcggtttctg aggtttcttca ctgcgcactg acggagctgc ggtggcgtct 60

ccacacgcaa cc atg aag ttg aag gac aca aaa tca agg cca aag cag tca 111
Met Lys Leu Lys Asp Thr Lys Ser Arg Pro Lys Gln Ser
1 5 10

agc tgt ggc aaa ttt cag aca aag gga atc aaa gtt gtg gga aaa tgg 159

240	245	250	
gcg gtg ttg cag tgg cag aag agg aat gct gcc cct cct cca agt aac Ala Val Leu Gln Trp Gln Lys Arg Asn Ala Ala Pro Pro Pro Ser Asn 255 260 265			879
acc gaa gca cca cct gga gag acc aga act gag gcc gga gct gag act Thr Glu Ala Pro Pro Gly Glu Thr Arg Thr Glu Ala Gly Ala Glu Thr 270 275 280 285			927
aga tca cca ggc aag gct gaa gct gag tct gat gca ttg cct gac gat Arg Ser Pro Gly Lys Ala Glu Ala Glu Ser Asp Ala Leu Pro Asp Asp 290 295 300			975
act gta att gag agt gaa gca ctg ccc agt gat att gca gcc gag gcc Thr Val Ile Glu Ser Glu Ala Leu Pro Ser Asp Ile Ala Ala Glu Ala 305 310 315			1023
aga gcc aag act gga ggc act gtc tca gac cag gcg ttg ctc ttt ggt Arg Ala Lys Thr Gly Gly Thr Val Ser Asp Gln Ala Leu Leu Phe Gly 320 325 330			1071
gac gat gat gct ggt gaa ggg cct tct tcc ctg atc agg gag aaa cct Asp Asp Asp Ala Gly Glu Gly Pro Ser Ser Leu Ile Arg Glu Lys Pro 335 340 345			1119
gtt ccc aaa cag aat gag aat gag gag gaa aat ctt gat aaa gag cag Val Pro Lys Gln Asn Glu Asn Glu Glu Glu Asn Leu Asp Lys Glu Gln 350 355 360 365			1167
act gga aat cta aaa cag gag ttg gat gac aaa agc gcc acc tgt aag Thr Gly Asn Leu Lys Gln Glu Leu Asp Asp Lys Ser Ala Thr Cys Lys 370 375 380			1215
gca tat cca aag cgt cct ctg ctt gga ctg gtt ctg act ccc act cga Ala Tyr Pro Lys Arg Pro Leu Leu Gly Leu Val Leu Thr Pro Thr Arg 385 390 395			1263
gag ctg gcc gtc cag gtc aaa cag cac att gat gct gtg gcc agg ttt Glu Leu Ala Val Gln Val Lys Gln His Ile Asp Ala Val Ala Arg Phe 400 405 410			1311
aca gga att aaa act gct att ttg gtt ggt gga atg tcc acg cag aaa Thr Gly Ile Lys Thr Ala Ile Leu Val Gly Gly Met Ser Thr Gln Lys 415 420 425			1359
cag cag agg atg ctg aac cgt cgt cct gag att gtg gtt gct act cca Gln Gln Arg Met Leu Asn Arg Arg Pro Glu Ile Val Val Ala Thr Pro 430 435 440 445			1407
ggc cgg ctg tgg gaa tta att aaa gaa aag cat tat cat ttg agg aac Gly Arg Leu Trp Glu Leu Ile Lys Glu Lys His Tyr His Leu Arg Asn 450 455 460			1455
ctt cgg cag ctc agg tgc ctg gta gtg gat gag gct gac cgg atg gtt Leu Arg Gln Leu Arg Cys Leu Val Val Asp Glu Ala Asp Arg Met Val 465 470 475			1503

gag aaa ggc cat ttt gct gag ctc tca cag ctg cta gag atg ctc aat	1551
Glu Lys Gly His Phe Ala Glu Leu Ser Gln Leu Leu Glu Met Leu Asn	
480 485 490	
gac tcc caa tac aac cca aag aga caa acg ctt gtt ttt tct gcc aca	1599
Asp Ser Gln Tyr Asn Pro Lys Arg Gln Thr Leu Val Phe Ser Ala Thr	
495 500 505	
ctc acc ctg gtg cat cag gct cct gct cga atc ctt cat aag aag cac	1647
Leu Thr Leu Val His Gln Ala Pro Ala Arg Ile Leu His Lys Lys His	
510 515 520 525	
acc aag aaa atg gat aaa aca gcc aaa ctt gac ctc ctt atg cag aaa	1695
Thr Lys Lys Met Asp Lys Thr Ala Lys Leu Asp Leu Leu Met Gln Lys	
530 535 540	
att ggc atg agg ggc aag ccc aag gtc att gac ctc aca agg aat gag	1743
Ile Gly Met Arg Gly Lys Pro Lys Val Ile Asp Leu Thr Arg Asn Glu	
545 550 555	
gcc acg gtg gag acg cta aca gag acc aag atc cat tgt gag act gat	1791
Ala Thr Val Glu Thr Leu Thr Glu Thr Lys Ile His Cys Glu Thr Asp	
560 565 570	
gag aaa gac ttc tac ttg tac tac ttc ctg atg cag tat cca ggc cgc	1839
Glu Lys Asp Phe Tyr Leu Tyr Tyr Phe Leu Met Gln Tyr Pro Gly Arg	
575 580 585	
agc tta gtg ttt gcc aac agt atc tcc tgc atc aaa cgc ctc tct ggg	1887
Ser Leu Val Phe Ala Asn Ser Ile Ser Cys Ile Lys Arg Leu Ser Gly	
590 595 600 605	
ctc ctc aaa gtc ctt gat atc atg ccc ttg acc ctg cat gcc tgt atg	1935
Leu Leu Lys Val Leu Asp Ile Met Pro Leu Thr Leu His Ala Cys Met	
610 615 620	
cac cag aag cag agg ctc aga aac ctg gag cag ttt gcc cgt ctg gaa	1983
His Gln Lys Gln Arg Leu Arg Asn Leu Glu Gln Phe Ala Arg Leu Glu	
625 630 635	
gac tgt gtt ctc ttg gca aca gat gtg gca gct cgg ggt ctg gat att	2031
Asp Cys Val Leu Leu Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile	
640 645 650	
cct aaa gtc cag cat gtc atc cat tac cag gtc cca cgt acc tcg gag	2079
Pro Lys Val Gln His Val Ile His Tyr Gln Val Pro Arg Thr Ser Glu	
655 660 665	
att tat gtc cac cga agt ggt cga act gct cga gct acc aat gaa ggc	2127
Ile Tyr Val His Arg Ser Gly Arg Thr Ala Arg Ala Thr Asn Glu Gly	
670 675 680 685	
ctc agt ctg atg ctc att ggg cct gag gat gtg atc aac ttt aag aag	2175
Leu Ser Leu Met Leu Ile Gly Pro Glu Asp Val Ile Asn Phe Lys Lys	
690 695 700	

att tac aaa acg ctc aag aaa gat gag gat atc cca ctg ttc ccc gtg 2223
 ile Tyr Lys Thr Leu Lys Lys Asp Glu Asp Ile Pro Leu Phe Pro Val
 705 710 715

cag aca aaa tac atg gat gtg gtc aag gag cga atc cgt tta gct cga 2271
 Gln Thr Lys Tyr Met Asp Val Val Lys Glu Arg Ile Arg Leu Ala Arg
 720 725 730

cag att gag aaa tct gag tat cgg aac ttc cag gct tgc ctg cac aac 2319
 Gln Ile Glu Lys Ser Glu Tyr Arg Asn Phe Gln Ala Cys Leu His Asn
 735 740 745

tct tgg att gag cag gca gca gct gcc ctg gag att gag ctg gaa gaa 2367
 Ser Trp Ile Glu Gln Ala Ala Ala Ala Leu Glu Ile Glu Leu Glu Glu
 750 755 760 765

gac atg tat aag gga gga aaa gct gac cag caa gaa gaa cgt cgg aga 2415
 Asp Met Tyr Lys Gly Gly Lys Ala Asp Gln Gln Glu Glu Arg Arg Arg
 770 775 780

caa aag cag atg aag gtt ctg aag aag gag ctg cgc cac ctg ctg tcc 2463
 Gln Lys Gln Met Lys Val Leu Lys Lys Glu Leu Arg His Leu Leu Ser
 785 790 795

cag cca ctg ttt acg gag agc cag aaa acc aag tat ccc act cag tct 2511
 Gln Pro Leu Phe Thr Glu Ser Gln Lys Thr Lys Tyr Pro Thr Gln Ser
 800 805 810

ggc aag ccg ccc ctg ctt gtg tct gcc cca agt aag agc gag tct gct 2559
 Gly Lys Pro Pro Leu Leu Val Ser Ala Pro Ser Lys Ser Glu Ser Ala
 815 820 825

ttg agc tgt ctc tcc aag cag aag aag aag aag aca aag aag ccg aag 2607
 Leu Ser Cys Leu Ser Lys Gln Lys Lys Lys Lys Thr Lys Lys Pro Lys
 830 835 840 845

gag cca cag ccg gaa cag cca cag cca agt aca agt gca aat taa 2652
 Glu Pro Gln Pro Glu Gln Pro Gln Pro Ser Thr Ser Ala Asn
 850 855

ctgggtcaagt gtgtcagtga ctgcacattg gtttctgttc tctggctatt tgcaaaacct 2712

ctccccacct tgtgttttcac tccaccacca accccaggta aaaaagtctc cctctcttcc 2772

actcacacccc atagcggggag agacctcatg cagatttgca ttgttttgga gtaagaattc 2832

aatgcagcag cttaattttt ctgtattgca gtgttttatag gcttcttgtg tgttaaactt 2892

gatttcataa attaaaaaca atgggtcag 2920

<210> 38
 <211> 859
 <212> PRT
 <213> Homo sapiens

<400> 38
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			20					25					30		
Lys	Ile	Asp	Pro	Asn	Met	Phe	Ala	Asp	Gly	Gln	Met	Asp	Asp	Leu	Val
		35					40					45			
Cys	Phe	Glu	Glu	Leu	Thr	Asp	Tyr	Gln	Leu	Val	Ser	Pro	Ala	Lys	Asn
	50					55					60				
Pro	Ser	Ser	Leu	Phe	Ser	Lys	Glu	Ala	Pro	Lys	Arg	Lys	Ala	Gln	Ala
	65				70					75				80	
Val	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Lys	Ser	Ser	Ser	Pro	Lys
			85					90						95	
Lys	Lys	Ile	Lys	Leu	Lys	Lys	Ser	Lys	Asn	Val	Ala	Thr	Glu	Gly	Thr
			100					105					110		
Ser	Thr	Gln	Lys	Glu	Phe	Glu	Val	Lys	Asp	Pro	Glu	Leu	Glu	Ala	Gln
		115					120					125			
Gly	Asp	Asp	Met	Val	Cys	Asp	Asp	Pro	Glu	Ala	Gly	Glu	Met	Thr	Ser
	130					135					140				
Glu	Asn	Leu	Val	Gln	Thr	Ala	Pro	Lys	Lys	Lys	Asn	Lys	Gly	Lys	
	145				150				155					160	
Lys	Gly	Leu	Glu	Pro	Ser	Gln	Ser	Thr	Ala	Ala	Lys	Val	Pro	Lys	Lys
				165				170						175	
Ala	Lys	Thr	Trp	Ile	Pro	Glu	Val	His	Asp	Gln	Lys	Ala	Asp	Val	Ser
			180					185					190		
Ala	Trp	Lys	Asp	Leu	Phe	Val	Pro	Arg	Pro	Val	Leu	Arg	Ala	Leu	Ser
		195					200					205			
Phe	Leu	Gly	Phe	Ser	Ala	Pro	Thr	Pro	Ile	Gln	Ala	Leu	Thr	Leu	Ala
	210					215				220					
Pro	Ala	Ile	Arg	Asp	Lys	Leu	Asp	Ile	Leu	Gly	Ala	Ala	Glu	Thr	Gly
	225			230				235						240	
Ser	Gly	Lys	Thr	Leu	Ala	Phe	Ala	Ile	Pro	Met	Ile	His	Ala	Val	Leu
			245					250					255		
Gln	Trp	Gln	Lys	Arg	Asn	Ala	Ala	Pro	Pro	Pro	Ser	Asn	Thr	Glu	Ala
			260					265					270		
Pro	Pro	Gly	Glu	Thr	Arg	Thr	Glu	Ala	Gly	Ala	Glu	Thr	Arg	Ser	Pro
		275					280					285			
Gly	Lys	Ala	Glu	Ala	Glu	Ser	Asp	Ala	Leu	Pro	Asp	Asp	Thr	Val	Ile
	290					295					300				
Glu	Ser	Glu	Ala	Leu	Pro	Ser	Asp	Ile	Ala	Ala	Glu	Ala	Arg	Ala	Lys
	305				310				315					320	
Thr	Gly	Gly	Thr	Val	Ser	Asp	Gln	Ala	Leu	Leu	Phe	Gly	Asp	Asp	Asp
			325					330					335		
Ala	Gly	Glu	Gly	Pro	Ser	Ser	Leu	Ile	Arg	Glu	Lys	Pro	Val	Pro	Lys
			340					345					350		
Gln	Asn	Glu	Asn	Glu	Glu	Glu	Asn	Leu	Asp	Lys	Glu	Gln	Thr	Gly	Asn
	355						360					365			
Leu	Lys	Gln	Glu	Leu	Asp	Asp	Lys	Ser	Ala	Thr	Cys	Lys	Ala	Tyr	Pro
	370				375						380				
Lys	Arg	Pro	Leu	Leu	Gly	Leu	Val	Leu	Thr	Pro	Thr	Arg	Glu	Leu	Ala
	385				390					395				400	
Val	Gln	Val	Lys	Gln	His	Ile	Asp	Ala	Val	Ala	Arg	Phe	Thr	Gly	Ile
			405					410					415		
Lys	Thr	Ala	Ile	Leu	Val	Gly	Gly	Met	Ser	Thr	Gln	Lys	Gln	Gln	Arg
			420				425						430		
Met	Leu	Asn	Arg	Arg	Pro	Glu	Ile	Val	Val	Ala	Thr	Pro	Gly	Arg	Leu
	435					440						445			
Trp	Glu	Leu	Ile	Lys	Glu	Lys	His	Tyr	His	Leu	Arg	Asn	Leu	Arg	Gln
	450					455					460				

Leu Arg Cys Leu Val Val Asp Glu Ala Asp Arg Met Val Glu Lys Gly
 465 470 475 480
 His Phe Ala Glu Leu Ser Gln Leu Leu Glu Met Leu Asn Asp Ser Gln
 485 490 495
 Tyr Asn Pro Lys Arg Gln Thr Leu Val Phe Ser Ala Thr Leu Thr Leu
 500 505 510
 Val His Gln Ala Pro Ala Arg Ile Leu His Lys Lys His Thr Lys Lys
 515 520 525
 Met Asp Lys Thr Ala Lys Leu Asp Leu Leu Met Gln Lys Ile Gly Met
 530 535 540
 Arg Gly Lys Pro Lys Val Ile Asp Leu Thr Arg Asn Glu Ala Thr Val
 545 550 555 560
 Glu Thr Leu Thr Glu Thr Lys Ile His Cys Glu Thr Asp Glu Lys Asp
 565 570 575
 Phe Tyr Leu Tyr Tyr Phe Leu Met Gln Tyr Pro Gly Arg Ser Leu Val
 580 585 590
 Phe Ala Asn Ser Ile Ser Cys Ile Lys Arg Leu Ser Gly Leu Leu Lys
 595 600 605
 Val Leu Asp Ile Met Pro Leu Thr Leu His Ala Cys Met His Gln Lys
 610 615 620
 Gln Arg Leu Arg Asn Leu Glu Gln Phe Ala Arg Leu Glu Asp Cys Val
 625 630 635 640
 Leu Leu Ala Thr Asp Val Ala Ala Arg Gly Leu Asp Ile Pro Lys Val
 645 650 655
 Gln His Val Ile His Tyr Gln Val Pro Arg Thr Ser Glu Ile Tyr Val
 660 665 670
 His Arg Ser Gly Arg Thr Ala Arg Ala Thr Asn Glu Gly Leu Ser Leu
 675 680 685
 Met Leu Ile Gly Pro Glu Asp Val Ile Asn Phe Lys Lys Ile Tyr Lys
 690 695 700
 Thr Leu Lys Lys Asp Glu Asp Ile Pro Leu Phe Pro Val Gln Thr Lys
 705 710 715 720
 Tyr Met Asp Val Val Lys Glu Arg Ile Arg Leu Ala Arg Gln Ile Glu
 725 730 735
 Lys Ser Glu Tyr Arg Asn Phe Gln Ala Cys Leu His Asn Ser Trp Ile
 740 745 750
 Glu Gln Ala Ala Ala Ala Leu Glu Ile Glu Leu Glu Glu Asp Met Tyr
 755 760 765
 Lys Gly Gly Lys Ala Asp Gln Gln Glu Glu Arg Arg Arg Gln Lys Gln
 770 775 780
 Met Lys Val Leu Lys Lys Glu Leu Arg His Leu Leu Ser Gln Pro Leu
 785 790 795 800
 Phe Thr Glu Ser Gln Lys Thr Lys Tyr Pro Thr Gln Ser Gly Lys Pro
 805 810 815
 Pro Leu Leu Val Ser Ala Pro Ser Lys Ser Glu Ser Ala Leu Ser Cys
 820 825 830
 Leu Ser Lys Gln Lys Lys Lys Lys Thr Lys Lys Pro Lys Glu Pro Gln
 835 840 845
 Pro Glu Gln Pro Gln Pro Ser Thr Ser Ala Asn
 850 855

<210> 39
 <211> 1502
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (15)..(998)

<400> 39

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1 5 10	
tgc ggc cgt ggg tgg tcg cgg gcg atg cgg ggc tgc cag ctc ctc ggg	98
Cys Gly Arg Gly Trp Ser Arg Ala Met Arg Gly Cys Gln Leu Leu Gly	
15 20 25	
ctt cgt agc tct tgg ccc ggg gac cta cta agt gct cgg ctc ttg tcc	146
Leu Arg Ser Ser Trp Pro Gly Asp Leu Leu Ser Ala Arg Leu Leu Ser	
30 35 40	
caa gag aag cgg gca gcg gaa acg cac ttt ggg ttt gag act gtg tcg	194
Gln Glu Lys Arg Ala Ala Glu Thr His Phe Gly Phe Glu Thr Val Ser	
45 50 55 60	
gaa gag gag aag ggg ggc aaa gtc tat cag gtg ttt gaa agt gtg gct	242
Glu Glu Glu Lys Gly Gly Lys Val Tyr Gln Val Phe Glu Ser Val Ala	
65 70 75	
aag aag tat gat gtg atg aat gat atg atg agt ctt ggt atc cat cgt	290
Lys Lys Tyr Asp Val Met Asn Asp Met Met Ser Leu Gly Ile His Arg	
80 85 90	
gtt tgg aag gat ttg ctg ctc tgg aag atg cac ccg ctt cct ggg acc	338
Val Trp Lys Asp Leu Leu Leu Trp Lys Met His Pro Leu Pro Gly Thr	
95 100 105	
cag ctg ctt gat gtt gct gga ggc aca ggt gac att gca ttc cgg ttc	386
Gln Leu Leu Asp Val Ala Gly Gly Thr Gly Asp Ile Ala Phe Arg Phe	
110 115 120	
ctt aat tat gtt cag tcc cag cat cag aga aaa cag aag agg cag tta	434
Leu Asn Tyr Val Gln Ser Gln His Gln Arg Lys Gln Lys Arg Gln Leu	
125 130 135 140	
agg gcc caa caa aat tta tcc tgg gaa gaa att gcc aaa gag tac cag	482
Arg Ala Gln Gln Asn Leu Ser Trp Glu Glu Ile Ala Lys Glu Tyr Gln	
145 150 155	
aat gaa gaa gat tcc ttg ggc ggg tct cgt gtc gtg gtg tgt gac atc	530
Asn Glu Glu Asp Ser Leu Gly Gly Ser Arg Val Val Val Cys Asp Ile	
160 165 170	
aac aag gag atg cta aag gtt gga aag cag aaa gcc ttg gct caa gga	578
Asn Lys Glu Met Leu Lys Val Gly Lys Gln Lys Ala Leu Ala Gln Gly	
175 180 185	
tac aga gct gga ctt gca tgg gta tta gga gat gct gaa gaa ctg ccc	626
Tyr Arg Ala Gly Leu Ala Trp Val Leu Gly Asp Ala Glu Glu Leu Pro	
190 195 200	

ttt gat gat gac aag ttt gat att tac acc att gcc ttt ggg atc cgg	674
Phe Asp Asp Asp Lys Phe Asp Ile Tyr Thr Ile Ala Phe Gly Ile Arg	
205 210 215 220	
aat gtc aca cac att gat cag gca ctc cag gaa gct cat cgg gtg ctg	722
Asn Val Thr His Ile Asp Gln Ala Leu Gln Glu Ala His Arg Val Leu	
225 230 235	
aaa cca gga gga cgg ttt ctc tgt ctg gaa ttt agc caa gtg aac aat	770
Lys Pro Gly Gly Arg Phe Leu Cys Leu Glu Phe Ser Gln Val Asn Asn	
240 245 250	
ccc ctc ata tcc agg ctt tat gat cta tat agc ttc cag gtc atc cct	818
Pro Leu Ile Ser Arg Leu Tyr Asp Leu Tyr Ser Phe Gln Val Ile Pro	
255 260 265	
gtc ctg gga gag gtc atc gct gga gac tgg aag tcc tat cag tac ctt	866
Val Leu Gly Glu Val Ile Ala Gly Asp Trp Lys Ser Tyr Gln Tyr Leu	
270 275 280	
gta gag agt atc cga agg ttt ccg tct cag gaa gag ttc aag gac atg	914
Val Glu Ser Ile Arg Arg Phe Pro Ser Gln Glu Glu Phe Lys Asp Met	
285 290 295 300	
ata gaa gat gca ggc ttt cac aag gtg act tac gaa agt cta aca tca	962
Ile Glu Asp Ala Gly Phe His Lys Val Thr Tyr Glu Ser Leu Thr Ser	
305 310 315	
ggc att gtg gcc att cat tct ggc ttc aaa ctt taa ttcctttcct	1008
Gly Ile Val Ala Ile His Ser Gly Phe Lys Leu	
320 325	
atcatggagc atgaaccagt catatcctgt tgaaagcctg gaactgaagg ataatctggc	1068
aaatgagaca gcagcagagc atctcctctt aaggatacgt gccttggact catgtttgaa	1128
tcgaacagtc tcaaagtgga agaacaaatt cttgtcactt ttttacagct ttctttggag	1188
ctgcttcagt ccatctccca gaggcatttg gtctgtatct ttgctcaact gctaatttct	1248
cttggtctgta ggggtgtgtgg ttaaggtaca accacccta aagctcagtt ttgaagtgag	1308
tgtatttata gcttctctgc tgggtctgcc ttctagaggg atgatagatc atttgaacct	1368
aatgacaatt tttaaccaga aaatttaatt gtacctgaat caacctttca gcctaggacg	1428
aagtctaggc ccaagtcaga gtattaatga tcatgagaat tgtgtgctga accagtaaac	1488
gagtttacct ttg	1502

<210> 40
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 40

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Trp	Ser	Arg	Ala	Met	Arg	Gly	Cys	Gln	Leu	Leu	Gly	Leu	Arg	Ser	Ser
			20					25					30		
Trp	Pro	Gly	Asp	Leu	Leu	Ser	Ala	Arg	Leu	Leu	Ser	Gln	Glu	Lys	Arg
			35				40					45			
Ala	Ala	Glu	Thr	His	Phe	Gly	Phe	Glu	Thr	Val	Ser	Glu	Glu	Glu	Lys
			50			55					60				
Gly	Gly	Lys	Val	Tyr	Gln	Val	Phe	Glu	Ser	Val	Ala	Lys	Lys	Tyr	Asp
65					70					75					80
Val	Met	Asn	Asp	Met	Met	Ser	Leu	Gly	Ile	His	Arg	Val	Trp	Lys	Asp
				85					90					95	
Leu	Leu	Leu	Trp	Lys	Met	His	Pro	Leu	Pro	Gly	Thr	Gln	Leu	Leu	Asp
			100					105					110		
Val	Ala	Gly	Gly	Thr	Gly	Asp	Ile	Ala	Phe	Arg	Phe	Leu	Asn	Tyr	Val
			115				120					125			
Gln	Ser	Gln	His	Gln	Arg	Lys	Gln	Lys	Arg	Gln	Leu	Arg	Ala	Gln	Gln
			130			135					140				
Asn	Leu	Ser	Trp	Glu	Glu	Ile	Ala	Lys	Glu	Tyr	Gln	Asn	Glu	Glu	Asp
145					150					155					160
Ser	Leu	Gly	Gly	Ser	Arg	Val	Val	Val	Cys	Asp	Ile	Asn	Lys	Glu	Met
				165					170					175	
Leu	Lys	Val	Gly	Lys	Gln	Lys	Ala	Leu	Ala	Gln	Gly	Tyr	Arg	Ala	Gly
			180					185					190		
Leu	Ala	Trp	Val	Leu	Gly	Asp	Ala	Glu	Glu	Leu	Pro	Phe	Asp	Asp	Asp
			195				200					205			
Lys	Phe	Asp	Ile	Tyr	Thr	Ile	Ala	Phe	Gly	Ile	Arg	Asn	Val	Thr	His
			210			215					220				
Ile	Asp	Gln	Ala	Leu	Gln	Glu	Ala	His	Arg	Val	Leu	Lys	Pro	Gly	Gly
225					230					235					240
Arg	Phe	Leu	Cys	Leu	Glu	Phe	Ser	Gln	Val	Asn	Asn	Pro	Leu	Ile	Ser
				245					250					255	
Arg	Leu	Tyr	Asp	Leu	Tyr	Ser	Phe	Gln	Val	Ile	Pro	Val	Leu	Gly	Glu
			260					265					270		
Val	Ile	Ala	Gly	Asp	Trp	Lys	Ser	Tyr	Gln	Tyr	Leu	Val	Glu	Ser	Ile
			275				280					285			
Arg	Arg	Phe	Pro	Ser	Gln	Glu	Glu	Phe	Lys	Asp	Met	Ile	Glu	Asp	Ala
			290			295					300				
Gly	Phe	His	Lys	Val	Thr	Tyr	Glu	Ser	Leu	Thr	Ser	Gly	Ile	Val	Ala
305					310					315					320
Ile	His	Ser	Gly	Phe	Lys	Leu									
				325											

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (127)..(387)

<400> 41
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 aaaacgctag agcggcgagt tgttacctgc gtcctctgac ctgagagcga aggggaaagc 120

Table 1. Demographic characteristics of the study population	
Age (years)	50.0 ± 10.0
Gender	
Male	50.0%
Female	50.0%
Education (years)	12.0 ± 2.0
Marital status	
Married	80.0%
Single	20.0%
Occupation	
Professional	30.0%
Managerial	20.0%
Technical	10.0%
Service	20.0%
Unemployed	20.0%
Income (USD/month)	1000.0 ± 500.0
Health status	
Good	70.0%
Fair	20.0%
Poor	10.0%

<400> 43
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caa cag ctg aaa caa att atg gat caa tta cga aat ctc atc tgg gat 591
Gln Gln Leu Lys Gln Ile Met Asp Gln Leu Arg Asn Leu Ile Trp Asp
155 160 165

ata aat gcc atg ttg gca atg agg aac taa gctgatattt aaatttcctg 641
 Ile Asn Ala Met Leu Ala Met Arg Asn
 170 175

ctttacacat gttataccat tgttttttcc ctcaagtatt ttttcctgt gaagaagatt 701
 atttatctgc ttttatttta gtcactaaaa cttaaagtttt tattttttaca ttgtgatttt 761
 tacattaaaa tattaacttt ttttaagtct attttatgaa agattattgt aataaacttt 821
 gatgggggtt gtatttttgt taatcttcat gaattgaata attgtttttt taaagcaaaa 881
 taaagttttt taaataaatg tt 903

<210> 44
 <211> 178
 <212> PRT
 <213> Homo sapiens

<400> 44
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 Leu Cys Arg Ile Gly Gln Glu Thr Val Gln Asp Ile Val Tyr Arg Thr
 35 40 45
 Met Glu Ile Phe Gln Leu Leu Arg Asn Met Gln Leu Pro Asn Gly Val
 50 55 60
 Thr Tyr His Thr Gly Thr Tyr Gln Asp Arg Leu Thr Lys Leu Gln Asp
 65 70 75 80
 Asn Leu Arg Gln Leu Ser Val Leu Phe Arg Lys Leu Arg Leu Val Tyr
 85 90 95
 Asp Lys Cys Asn Glu Asn Cys Gly Gly Met Asp Pro Ile Pro Val Glu
 100 105 110
 Gln Leu Ile Pro Tyr Val Glu Glu Asp Gly Ser Lys Asn Asp Asp Arg
 115 120 125
 Ala Gly Pro Pro Arg Phe Ala Ser Glu Glu Arg Arg Glu Ile Ala Glu
 130 135 140
 Val Asn Lys Lys Leu Lys Gln Lys Asn Gln Gln Leu Lys Gln Ile Met
 145 150 155 160
 Asp Gln Leu Arg Asn Leu Ile Trp Asp Ile Asn Ala Met Leu Ala Met
 165 170 175
 Arg Asn

<210> 45
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (187)..(540)

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ccaagatcct ttcaggatat ttggtttttt gggcgcgaca caaatcgagg tgaggggaaga 120

gagaggaaaa tcccctgaat ccctgcagga ttaatttatt caaaaaggaa ataaaaaata 180

ctcaat atg caa aag tct tgt gaa gaa aat gag gga aaa cca cag aac 228
Met Gln Lys Ser Cys Glu Glu Asn Glu Gly Lys Pro Gln Asn
1 5 10

atg cca aag gcc gag gaa gat cgc cct ttg gag gat gta cca cag gag 276
Met Pro Lys Ala Glu Glu Asp Arg Pro Leu Glu Asp Val Pro Gln Glu
15 20 25 30

gca gaa gga aat cct caa cct tcc gaa gaa ggc gta agc cag gaa gca 324
Ala Glu Gly Asn Pro Gln Pro Ser Glu Glu Gly Val Ser Gln Glu Ala
35 40 45

gaa gga aac ccc aga gga ggg ccg aat cag cct ggc cag gga ttt aaa 372
Glu Gly Asn Pro Arg Gly Gly Pro Asn Gln Pro Gly Gln Gly Phe Lys
50 55 60

gag gac aca ccc gtt agg cat ttg gac cct gaa gaa atg ata aga gga 420
Glu Asp Thr Pro Val Arg His Leu Asp Pro Glu Glu Met Ile Arg Gly
65 70 75

gta gat gag ctt gaa agg ctt agg gaa gag ata aga aga gta aga aac 468
Val Asp Glu Leu Glu Arg Leu Arg Glu Glu Ile Arg Arg Val Arg Asn
80 85 90

aag ttt gtg atg atg cat tgg aag caa aga cat tca cgc agc cgt cct 516
Lys Phe Val Met Met His Trp Lys Gln Arg His Ser Arg Ser Arg Pro
95 100 105 110

tat cct gtg tgc ttt agg cct tga attcattttt gcctaataatt aaaatctggc 570
Tyr Pro Val Cys Phe Arg Pro
115

cccagctttc tttctgtag cattttctga tgtatctttg acctccattt tacttttaat 630

catctgatga aattttgttt taggtaattt ccttggtacc agcatctcat tggatttttg 690

attttgaccc attttccagg tctatttttc aattggaaac tttcacacat ttgcatggga 750

atatgttcat tccatgttgt aaagtaaaac ataacagggt atggcaaagc agcatattta 810

atatcagctc acatatgtag gataaaattc caaactttgt gtgtgtgct gtgtgtatac 870

atacatccat ataacatata tcacaaactt aaccaagctt atttctgtgt ggtgtgaaat 930

tttatttggt ttcttctttt tgttcttttt gcttatatgt actttttaat gaacacgtgt 990

ctcacacaca aaaagaatta aggatttttt ttacaagtaa gagtcaaata atttgcaacc 1050

agcttatgag ggcaatgggg gcacctaaac tcttgatgaa agaactttaa aaagaaatgt 1110

aaacctcaaa ttacctctgg atctcttagc cagaggaata aactggcaat tattacagat 1170

<210> 46
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 46
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 Gly Asn Pro Gln Pro Ser Glu Glu Gly Val Ser Gln Glu Ala Glu Gly
 35 40 45
 Asn Pro Arg Gly Gly Pro Asn Gln Pro Gly Gln Gly Phe Lys Glu Asp
 50 55 60
 Thr Pro Val Arg His Leu Asp Pro Glu Glu Met Ile Arg Gly Val Asp
 65 70 75 80
 Glu Leu Glu Arg Leu Arg Glu Glu Ile Arg Arg Val Arg Asn Lys Phe
 85 90 95
 Val Met Met His Trp Lys Gln Arg His Ser Arg Ser Arg Pro Tyr Pro
 100 105 110
 Val Cys Phe Arg Pro
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<210> 47
 <211> 404
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (105)..(365)

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 Met Glu Leu Ser
 1
 gcc gaa tac ctc cgc gag aag ctg cag cgg gac ctg gag gcg gag cat 164
 Ala Glu Tyr Leu Arg Glu Lys Leu Gln Arg Asp Leu Glu Ala Glu His
 5 10 15 20
 gtg gag gtg gag gac acg acc ctc aac cgt tgc tcc tgt agc ttc cga 212
 Val Glu Val Glu Asp Thr Thr Leu Asn Arg Cys Ser Cys Ser Phe Arg
 25 30 35
 gtc ctg gtg gtg tcg gcc aag ttc gag ggg aaa ccg ctg ctt cag aga 260
 Val Leu Val Val Ser Ala Lys Phe Glu Gly Lys Pro Leu Leu Gln Arg
 40 45 50
 cac agg ctg gtg aac gcg tgc cta gca gaa gag ctc ccg cac atc cat 308
 His Arg Leu Val Asn Ala Cys Leu Ala Glu Glu Leu Pro His Ile His
 55 60 65

gcc ttt gaa cag aaa acc ctg acc cca gac cag tgg gca cgt gag cga 356
Ala Phe Glu Gln Lys Thr Leu Thr Pro Asp Gln Trp Ala Arg Glu Arg
70 75 80

cag aaa tga gggactggga tctgcacagc cattaata taaatctgg 404
Gln Lys
85

<210> 48
<211> 86
<212> PRT
<213> Homo sapiens

<400> 48
Met Glu Leu Ser Ala Glu Tyr Leu Arg Glu Lys Leu Gln Arg Asp Leu
1 5 10 15
Glu Ala Glu His Val Glu Val Glu Asp Thr Thr Leu Asn Arg Cys Ser
20 25 30
Cys Ser Phe Arg Val Leu Val Val Ser Ala Lys Phe Glu Gly Lys Pro
35 40 45
Leu Leu Gln Arg His Arg Leu Val Asn Ala Cys Leu Ala Glu Glu Leu
50 55 60
Pro His Ile His Ala Phe Glu Gln Lys Thr Leu Thr Pro Asp Gln Trp
65 70 75 80
Ala Arg Glu Arg Gln Lys
85

<210> 49
<211> 752
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (95)..(634)

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taccggacaa agagtgcgc cggagctgg agtt atg gcg gct acg gag ccg atc 115
Met Ala Ala Thr Glu Pro Ile
1 5

ttg gcg gcc act ggg agt ccc gcg gcg gtg cca ccg gag aaa ctg gaa 163
Leu Ala Ala Thr Gly Ser Pro Ala Ala Val Pro Pro Glu Lys Leu Glu
10 15 20

gga gcc ggt tcg agc tca gcc cct gag cgt aac tgt gtg ggc tcc tcg 211
Gly Ala Gly Ser Ser Ser Ala Pro Glu Arg Asn Cys Val Gly Ser Ser
25 30 35

ctg cca gag gcc tca ccg cct gcc cct gag cct tcc agt ccc aac gcc 259
Leu Pro Glu Ala Ser Pro Pro Ala Pro Glu Pro Ser Ser Pro Asn Ala
40 45 50 55

gcg gtc cct gaa gcc atc cct acg ccc cga gct gcg gcc tcc gcg gcc 307
 Ala Val Pro Glu Ala Ile Pro Thr Pro Arg Ala Ala Ser Ala Ala
 60 65 70

ctg gag ctg cct ctc ggg ccc gca ccc gtg agc gta gcg cct cag gcc 355
 Leu Glu Leu Pro Leu Gly Pro Ala Pro Val Ser Val Ala Pro Gln Ala
 75 80 85

gaa gct gaa gcg cgc tcc aca cca ggc ccc gcc ggc tct aga ctc ggt 403
 Glu Ala Glu Ala Arg Ser Thr Pro Gly Pro Ala Gly Ser Arg Leu Gly
 90 95 100

ccc gag acg ttc cgc cag cgt ttc cgg cag ttc cgc tac cag gat gcg 451
 Pro Glu Thr Phe Arg Gln Arg Phe Arg Gln Phe Arg Tyr Gln Asp Ala
 105 110 115

gcg ggt ccc cgg gag gct ttc cgg cag ctg cgg gag ctg tcc cgc cag 499
 Ala Gly Pro Arg Glu Ala Phe Arg Gln Leu Arg Glu Leu Ser Arg Gln
 120 125 130 135

tgg ctg cgg cct gac atc cgc acc aag gag cag atc gtg gag atg ctg 547
 Trp Leu Arg Pro Asp Ile Arg Thr Lys Glu Gln Ile Val Glu Met Leu
 140 145 150

gtg caa gag cag ctg ctc gcc atc ctg ccc gag gcg gct cgg gcc cgg 595
 Val Gln Glu Gln Leu Leu Ala Ile Leu Pro Glu Ala Ala Arg Ala Arg
 155 160 165

cgg atc cgc cgc cgc acg gat gtg cgc atc act ggc tga gcggtggagc 644
 Arg Ile Arg Arg Arg Thr Asp Val Arg Ile Thr Gly
 170 175

tgcgggcggc cagggccggg cgctctgtgc ggactggggc catgatcggg cccggggggcc 704

tgagcctggg accccacccc gtgttaatga aaaatgagtt ttggcagc 752

<210> 50
 <211> 179
 <212> PRT
 <213> Homo sapiens

<400> 50
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 Val Pro Pro Glu Lys Leu Glu Gly Ala Gly Ser Ser Ser Ala Pro Glu
 20 25 30
 Arg Asn Cys Val Gly Ser Ser Leu Pro Glu Ala Ser Pro Pro Ala Pro
 35 40 45
 Glu Pro Ser Ser Pro Asn Ala Ala Val Pro Glu Ala Ile Pro Thr Pro
 50 55 60
 Arg Ala Ala Ala Ser Ala Ala Leu Glu Leu Pro Leu Gly Pro Ala Pro
 65 70 75 80
 Val Ser Val Ala Pro Gln Ala Glu Ala Glu Ala Arg Ser Thr Pro Gly
 85 90 95
 Pro Ala Gly Ser Arg Leu Gly Pro Glu Thr Phe Arg Gln Arg Phe Arg
 100 105 110

Gln Phe Arg Tyr Gln Asp Ala Ala Gly Pro Arg Glu Ala Phe Arg Gln
 115 120 125
 Leu Arg Glu Leu Ser Arg Gln Trp Leu Arg Pro Asp Ile Arg Thr Lys
 130 135 140
 Glu Gln Ile Val Glu Met Leu Val Gln Glu Gln Leu Leu Ala Ile Leu
 145 150 155 160
 Pro Glu Ala Ala Arg Ala Arg Arg Ile Arg Arg Arg Thr Asp Val Arg
 165 170 175
 Ile Thr Gly

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 <211> 1222
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (219)..(788)

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 ctgaccgcgt gatccgccc cctcggcctc cgaaactgct gaaattacag gcgtgagcca 180
 ccgcgcccgg ccctccctct tccgctgccg ccgtggga atg gaa aca tct gcc cca 236
 Met Glu Thr Ser Ala Pro
 1 5
 cgt gcc gga agc caa gtg gtg gcg aca act gcg cgc cac tcc gcg gcc 284
 Arg Ala Gly Ser Gln Val Val Ala Thr Thr Ala Arg His Ser Ala Ala
 10 15 20
 tac cgc gca gat cct cta cgt gtg tcc tcg cga gac aag ctc acc gaa 332
 Tyr Arg Ala Asp Pro Leu Arg Val Ser Ser Arg Asp Lys Leu Thr Glu
 25 30 35
 atg gcc gcg tcc agt caa gga aac ttt gag gga aat ttt gag tca ctg 380
 Met Ala Ala Ser Ser Gln Gly Asn Phe Glu Gly Asn Phe Glu Ser Leu
 40 45 50
 gac ctt gcg gaa ttt gct aag aag cag cca tgg tgg cgt aag ctg ttc 428
 Asp Leu Ala Glu Phe Ala Lys Lys Gln Pro Trp Trp Arg Lys Leu Phe
 55 60 65 70
 ggg cag gaa tct gga cct tca gca gaa aag tat agc gtg gca acc cag 476
 Gly Gln Glu Ser Gly Pro Ser Ala Glu Lys Tyr Ser Val Ala Thr Gln
 75 80 85
 ctg ttc att gga ggt gtc act gga tgg tgc aca ggt ttc ata ttc cag 524
 Leu Phe Ile Gly Gly Val Thr Gly Trp Cys Thr Gly Phe Ile Phe Gln
 90 95 100
 aag gtt gga aag ttg gct gca aca gct gtg gga ggt gga ttt ttt ctc 572
 Lys Val Gly Lys Leu Ala Ala Thr Ala Val Gly Gly Gly Phe Phe Leu

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105              110              115
ctt cag ctt gca aac cat act ggg tac atc aaa gtt gac tgg caa cga 620
Leu Gln Leu Ala Asn His Thr Gly Tyr Ile Lys Val Asp Trp Gln Arg
120              125              130

gtg gag aag gac atg aag aaa gcc aaa gag cag ctg aag atc cgt aag 668
Val Glu Lys Asp Met Lys Lys Ala Lys Glu Gln Leu Lys Ile Arg Lys
135              140              145

agc aat cag ata cct act gag gtc agg agc aaa gct gag gag gtg gtg 716
Ser Asn Gln Ile Pro Thr Glu Val Arg Ser Lys Ala Glu Glu Val Val
155              160              165

tca ttt gtg aag aag aat gtt cta gta act ggg gga ttt ttc gga ggc 764
Ser Phe Val Lys Lys Asn Val Leu Val Thr Gly Gly Phe Phe Gly Gly
170              175              180

ttt ctg ctt ggc atg gca tcc taa ggaagatgac ctcattgttca ttgttcctgg 818
Phe Leu Leu Gly Met Ala Ser
185

ttttttccag ccagcagcct ctacactcca tcataggaca tcgagtcctt cctcctcttc 878

tcccatgcct tcttcctgc catggcaaatt ctgagtggtt tctctaagca tctgctggta 938

caagtcaatg tggcaccatg agcttcatgg tggcagaaga gacaatagtc cttagctctc 998

ctcccagtac accccctact tggccagtct gtaggccaac aagaaggttc ctttaccctc 1058

atgcaagaca cttatgagaa cacattacaa gatggctgac cgtggaggat gaggatgcc 1118

tgaaagggttg tcccaaactg ttgatttgga aaagaaataa gcacatagat aaccttattg 1178

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<210> 52
 <211> 189
 <212> PRT
 <213> Homo sapiens

<400> 52

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20     25     30
Arg Asp Lys Leu Thr Glu Met Ala Ala Ser Ser Gln Gly Asn Phe Glu
35     40     45
Gly Asn Phe Glu Ser Leu Asp Leu Ala Glu Phe Ala Lys Lys Gln Pro
50     55     60
Trp Trp Arg Lys Leu Phe Gly Gln Glu Ser Gly Pro Ser Ala Glu Lys
65     70     75     80
Tyr Ser Val Ala Thr Gln Leu Phe Ile Gly Gly Val Thr Gly Trp Cys
85     90     95
Thr Gly Phe Ile Phe Gln Lys Val Gly Lys Leu Ala Ala Thr Ala Val
100    105    110

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Gly Gly Gly Phe Phe Leu Leu Gln Leu Ala Asn His Thr Gly Tyr Ile
 115 120 125
 Lys Val Asp Trp Gln Arg Val Glu Lys Asp Met Lys Lys Ala Lys Glu
 130 135 140
 Gln Leu Lys Ile Arg Lys Ser Asn Gln Ile Pro Thr Glu Val Arg Ser
 145 150 155 160
 Lys Ala Glu Glu Val Val Ser Phe Val Lys Lys Asn Val Leu Val Thr
 165 170 175
 Gly Gly Phe Phe Gly Gly Phe Leu Leu Gly Met Ala Ser
 180 185

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 <212> DNA
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 <222> (95)..(448)

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 Met Ile Ser Gly Leu Phe Met
 1 5
 tcg ttg tgc tgc gcc ggg agc cac cgc cct ccg gag aca ggg cag ctc 163
 Ser Leu Cys Cys Ala Gly Ser His Arg Pro Pro Glu Thr Gly Gln Leu
 10 15 20
 ccc tac gac cct agc gcc tcc gcc ctc cgc ggc ccc tct cct ctc ttc 211
 Pro Tyr Asp Pro Ser Ala Ser Ala Leu Arg Gly Pro Ser Pro Leu Phe
 25 30 35
 ctg ctc tgt ccc tcc ttc tcc atc agg gag cag cgt gac ttc agc gag 259
 Leu Leu Cys Pro Ser Phe Ser Ile Arg Glu Gln Arg Asp Phe Ser Glu
 40 45 50 55
 tcc cgc gag cac ctg gct aga cag tta aca agc acg tcc ttc cag cct 307
 Ser Arg Glu His Leu Ala Arg Gln Leu Thr Ser Thr Ser Phe Gln Pro
 60 65 70
 gag cca gcg cag gtt tgg gag ggg gct tcc tgg ccc ccc cca cgg tgt 355
 Glu Pro Ala Gln Val Trp Glu Gly Ala Ser Trp Pro Pro Pro Arg Cys
 75 80 85
 tcc agc ccc tcc tct ctt ccg ccc cct agt ctc cca ccc ttc cct ccc 403
 Ser Ser Pro Ser Ser Leu Pro Pro Ser Leu Pro Pro Phe Pro Pro
 90 95 100
 cgt agt gac caa ttc cta tct ctt ccc tct ccg cag gct caa tga 448
 Arg Ser Asp Gln Phe Leu Ser Leu Pro Ser Pro Gln Ala Gln
 105 110 115
 atcgaatgaa tgtgaacttc ttcattctgtg aaaaatcttt tttttttcca ttttgttctg 508

09890688-093701

<222> (26)..(922)

<400> 55

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			1					5								
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Val	Phe	Lys	Val	Gly	Asn	Arg	Phe	Gln	Thr	Ala	Arg	Phe	Tyr	Arg	Asp	
10					15					20					25	
gtc	ctg	ggg	atg	aag	gtt	ctg	cgg	cat	gag	gaa	ttt	gaa	gaa	ggc	tgc	148
Val	Leu	Gly	Met	Lys	Val	Leu	Arg	His	Glu	Glu	Phe	Glu	Glu	Gly	Cys	
				30					35					40		
aaa	gct	gcc	tgt	aat	ggg	cct	tat	gat	ggg	aaa	tgg	agt	aaa	aca	atg	196
Lys	Ala	Ala	Cys	Asn	Gly	Pro	Tyr	Asp	Gly	Lys	Trp	Ser	Lys	Thr	Met	
				45				50					55			
gtg	gga	ttt	ggg	cct	gag	gat	gat	cat	ttt	gtc	gca	gaa	ctg	act	tac	244
Val	Gly	Phe	Gly	Pro	Glu	Asp	Asp	His	Phe	Val	Ala	Glu	Leu	Thr	Tyr	
		60					65					70				
aat	tat	ggc	gtc	gga	gac	tac	aag	ctt	ggc	aat	gac	ttt	atg	gga	atc	292
Asn	Tyr	Gly	Val	Gly	Asp	Tyr	Lys	Leu	Gly	Asn	Asp	Phe	Met	Gly	Ile	
	75					80					85					
acg	ctc	gct	tct	agc	cag	gct	gtc	agc	aac	gcc	agg	aag	ctg	gag	tgg	340
Thr	Leu	Ala	Ser	Ser	Gln	Ala	Val	Ser	Asn	Ala	Arg	Lys	Leu	Glu	Trp	
90					95					100					105	
cca	ctg	acg	gaa	gtt	gca	gaa	ggt	gtt	ttt	gaa	acc	gag	gcc	ccg	gga	388
Pro	Leu	Thr	Glu	Val	Ala	Glu	Gly	Val	Phe	Glu	Thr	Glu	Ala	Pro	Gly	
				110				115						120		
gga	tat	aag	ttc	tat	ttg	cag	aat	cgc	agt	ctg	cct	cag	tca	gat	cct	436
Gly	Tyr	Lys	Phe	Tyr	Leu	Gln	Asn	Arg	Ser	Leu	Pro	Gln	Ser	Asp	Pro	
			125					130				135				
gta	tta	aaa	gta	act	cta	gca	gtg	tct	gat	ctt	caa	aag	tcc	ttg	aac	484
Val	Leu	Lys	Val	Thr	Leu	Ala	Val	Ser	Asp	Leu	Gln	Lys	Ser	Leu	Asn	
		140					145					150				
tac	tgg	tgt	aat	cta	ctg	gga	atg	aaa	att	tat	gaa	aaa	gat	gaa	gaa	532
Tyr	Trp	Cys	Asn	Leu	Leu	Gly	Met	Lys	Ile	Tyr	Glu	Lys	Asp	Glu	Glu	
	155					160					165					
aag	caa	agg	gct	ttg	ctg	ggc	tat	gct	gat	aac	cag	tgt	aag	ctg	gag	580
Lys	Gln	Arg	Ala	Leu	Leu	Gly	Tyr	Ala	Asp	Asn	Gln	Cys	Lys	Leu	Glu	
170					175				180						185	
cta	cag	ggc	gtc	aag	ggg	ggg	gtg	gac	cat	gca	gca	gct	ttt	gga	aga	628
Leu	Gln	Gly	Val	Lys	Gly	Gly	Val	Asp	His	Ala	Ala	Ala	Phe	Gly	Arg	
				190				195					200			
att	gcc	ttc	tct	tgc	ccc	cag	aaa	gag	ttg	cca	gac	tta	gaa	gac	ttg	676
Ile	Ala	Phe	Ser	Cys	Pro	Gln	Lys	Glu	Leu	Pro	Asp	Leu	Glu	Asp	Leu	

205	210	215	
atg aaa agg gag aac cag aag att ctg act ccc ctg gtg agc ctg gac			724
Met Lys Arg Glu Asn Gln Lys Ile Leu Thr Pro Leu Val Ser Leu Asp			
220	225	230	
acc cca ggg aaa gca aca gta cag gtg gtc att ctg gcc gac cct gac			772
Thr Pro Gly Lys Ala Thr Val Gln Val Val Ile Leu Ala Asp Pro Asp			
235	240	245	
gga cat gaa att tgc ttt gtc ggg gat gaa gca ttt cga gaa ctt tct			820
Gly His Glu Ile Cys Phe Val Gly Asp Glu Ala Phe Arg Glu Leu Ser			
250	255	260	265
aag atg gat cca gag gga agc aaa ttg ttg gat gat gca atg gca gca			868
Lys Met Asp Pro Glu Gly Ser Lys Leu Leu Asp Asp Ala Met Ala Ala			
270	275	280	
gat aaa agt gac gag tgg ttt gcc aaa cac aat aaa ccc aaa gct tca			916
Asp Lys Ser Asp Glu Trp Phe Ala Lys His Asn Lys Pro Lys Ala Ser			
285	290	295	
ggt taa cggaagacat gatgcagagc aagcctctgt gattcctgcc cagcacctgt			972
Gly			
gaggcctgac gtgtcagttc ccaataaatg ctcttctgat ttgtttcccg tacaggcaag			1032
gaggcttggg tagtgcagat ttgtgtatatt caatctttga aagctctgat gtaatttaga			1092
aatgaaatcc aatcatgagt ccaggtagag aacgcctgct gtaatctaca ctgttgctgg			1152
gactgcgcat tctgtatata actgtgttgg atgagtgaca gatgattgtc cagactagga			1212
cagcggcatg aacatgactt tggttgggat tgcggatagt tagggttacc tctgaatcgt			1272
gtagctttta tgagagcagc tgtgcaagtg aatccacatt aatgccttgt cgtggtgcc			1332
ttcccagcgc ctgacgatac gctcttctat tgtcttattc tggcaggttt tgacgtttta			1392
aattttttta agaaatttta ttccttgagc caaaagggtt ggtaaccac cccctctta			1452
cttgctttca cattttgagt gtccagagga aacagaaaagg aatgagtgtg tgacgttgct			1512
gcacgcctga ctctgtgcga gcttctttct gtgtatatat tttgttttat ttttttccgt			1572
gtatatTTTT aatcccgaca gaacatcatg tgagatttct ttaaaatgga ttaaacgatt			1632
tcttcagcct gaaaaaaaaag gttttgaaaa tgttttcttg tagttttggt tggttctaaa			1692
caacaaatag gttttaatca ctcgaaatgg aattatattg tgtattcatt gaataaattt			1752
tttttgaaag t			1763
<210> 56			
<211> 298			
<212> PRT			

<213> Homo sapiens

<400> 56

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Phe Gln Thr Ala Arg Phe Tyr Arg Asp Val Leu Gly Met Lys Val Leu
20 25 30
Arg His Glu Glu Phe Glu Glu Gly Cys Lys Ala Ala Cys Asn Gly Pro
35 40 45
Tyr Asp Gly Lys Trp Ser Lys Thr Met Val Gly Phe Gly Pro Glu Asp
50 55 60
Asp His Phe Val Ala Glu Leu Thr Tyr Asn Tyr Gly Val Gly Asp Tyr
65 70 75 80
Lys Leu Gly Asn Asp Phe Met Gly Ile Thr Leu Ala Ser Ser Gln Ala
85 90 95
Val Ser Asn Ala Arg Lys Leu Glu Trp Pro Leu Thr Glu Val Ala Glu
100 105 110
Gly Val Phe Glu Thr Glu Ala Pro Gly Gly Tyr Lys Phe Tyr Leu Gln
115 120 125
Asn Arg Ser Leu Pro Gln Ser Asp Pro Val Leu Lys Val Thr Leu Ala
130 135 140
Val Ser Asp Leu Gln Lys Ser Leu Asn Tyr Trp Cys Asn Leu Leu Gly
145 150 155 160
Met Lys Ile Tyr Glu Lys Asp Glu Glu Lys Gln Arg Ala Leu Leu Gly
165 170 175
Tyr Ala Asp Asn Gln Cys Lys Leu Glu Leu Gln Gly Val Lys Gly Gly
180 185 190
Val Asp His Ala Ala Ala Phe Gly Arg Ile Ala Phe Ser Cys Pro Gln
195 200 205
Lys Glu Leu Pro Asp Leu Glu Asp Leu Met Lys Arg Glu Asn Gln Lys
210 215 220
Ile Leu Thr Pro Leu Val Ser Leu Asp Thr Pro Gly Lys Ala Thr Val
225 230 235 240
Gln Val Val Ile Leu Ala Asp Pro Asp Gly His Glu Ile Cys Phe Val
245 250 255
Gly Asp Glu Ala Phe Arg Glu Leu Ser Lys Met Asp Pro Glu Gly Ser
260 265 270
Lys Leu Leu Asp Asp Ala Met Ala Ala Asp Lys Ser Asp Glu Trp Phe
275 280 285
Ala Lys His Asn Lys Pro Lys Ala Ser Gly
290 295

<210> 57

<211> 1913

<212> DNA

<213> Homo sapiens

<220>

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<400> 57

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gagactgtcc gaagactgct atctgggacg agacaagttg ttaaagggac aggagagaaa 180
gcagagctat ttcaagagtg agccacagaa gggaatccag aggccatcta agcgaggaag 240
ggctctacagg cagtgagtga aggccaggag cagggcccag gccaggcacg accaccgagg 300
gg atg aac ttc aca gtg ggt ttc aag ccg ctg cta ggg gat gca cac 347
Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu Gly Asp Ala His
1 5 10 15
agc atg gac aac ctg gag aag cag ctc atc tgc ccc atc tgc ctg gag 395
Ser Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu
20 25 30
atg ttc tcc aaa cca gtg gtg atc ctg ccc tgc caa cac aac ctg tgc 443
Met Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys
35 40 45
cgc aaa tgt gcc aac gac gtc ttc cag gcc tcg aat cct cta tgg cag 491
Arg Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln
50 55 60
tcc cgg ggc tcc acc act gtg tct tca gga ggc cgt ttc cgc tgc cca 539
Ser Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro
65 70 75
tcg tgc agg cat gag gtt gtc ctg gac aga cac ggt gtc tac ggc ctg 587
Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu
80 85 90 95
cag cga aac ctg cta gtg gag aac att atc gac att tac aag cag gag 635
Gln Arg Asn Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu
100 105 110
tca tcc agg ccg ctg cac tcc aag gct gag cag cac ctc atg tgc gag 683
Ser Ser Arg Pro Leu His Ser Lys Ala Glu Gln His Leu Met Cys Glu
115 120 125
gag cat gaa gaa gag aag atc aat att tac tgc ctg agc tgt gag gtg 731
Glu His Glu Glu Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val
130 135 140
ccc acc tgc tct ctc tgc aag gtc ttc ggt gcc cac aag gac tgt gag 779
Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu
145 150 155
gtg gcc cca ctg ccc acc att tac aaa cgc cag aag agt gag ctc agc 827
Val Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser
160 165 170 175
gat ggc atc gcg atg ctg gtg gca ggc aat gac cgc gtg caa gca gtg 875
Asp Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val
180 185 190
atc aca cag atg gag gag gtg tgc cag act atc gag gac aat agc cgg 923
Ile Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg

195	200	205	
agg cag aag cag ttg tta aac cag agg ttt gag agc ctg tgc gca gtg			971
Arg Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Ser Leu Cys Ala Val			
210	215	220	
ctg gag gag cgc aag ggt gag ctg ctg cag gcg ctg gcc cgg gag caa			1019
Leu Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln			
225	230	235	
gag gag aag ctg cag cgc gtc cgc ggc ctc atc cgt cag tat ggc gac			1067
Glu Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp			
240	245	250	255
cac ctg gag gcc tcc tct aag ctg gtg gag tct gcc atc cag tcc atg			1115
His Leu Glu Ala Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met			
260	265	270	
gaa gag cca caa atg gcg ctg tat ctc cag cag gcc aag gag ctg atc			1163
Glu Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile			
275	280	285	
aat aag gtc ggg gcc atg tcg aag gtg gag ctg gca ggg cgg ccg gag			1211
Asn Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu			
290	295	300	
cca ggc tat gag agc atg gag caa ttc acc gta agg gtg gag cac gtg			1259
Pro Gly Tyr Glu Ser Met Glu Gln Phe Thr Val Arg Val Glu His Val			
305	310	315	
gcc gaa atg ctg cgg acc atc gac ttc cag cca ggc gct tcc ggg gag			1307
Ala Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ser Gly Glu			
320	325	330	335
gaa gag gag gtg gcc cca gac gga gag gag ggc agc gcg ggg ccg gag			1355
Glu Glu Glu Val Ala Pro Asp Gly Glu Glu Gly Ser Ala Gly Pro Glu			
340	345	350	
gaa gag cgg ccg gat ggg cct taa ggccctgcgcc gacccgaccc tgctcgagag			1409
Glu Glu Arg Pro Asp Gly Pro			
355			
cccgcgctag agtcgggggag gatctgcgca gagaccgcag catcacccaa atcggcgccg			1469
gccccgggag gatctcaata aagaactcga gcgtcccaga cccgtatctc ctttcgctgc			1529
ccaaccccgcc agcctgggct tcgaaggcga cccgcccacc atcctgccct tcccagaacc			1589
tgagaccgtc tggggggcg aagccaaatg aaccctatt gggcacctct gtgatgccag			1649
gagcgaactg gtgagcccag cgccctggga agagggccga gggcggggag gtggtgccg			1709
gacctctgag gtccctggga tttggggacc cttgggggtcc acatgcacct ggctgacctg			1769
gctgaaagcc gctgtctcgg agccccccac agcattttgt tcccctcccg ctggccccggg			1829
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1913

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 <212> PRT
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<400> 58
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 Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
 35 40 45
 Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln Ser
 50 55 60
 Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro Ser
 65 70 75 80
 Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln
 85 90 95
 Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser
 100 105 110
 Ser Arg Pro Leu His Ser Lys Ala Glu Gln His Leu Met Cys Glu Glu
 115 120 125
 His Glu Glu Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val Pro
 130 135 140
 Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu Val
 145 150 155 160
 Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser Asp
 165 170 175
 Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val Ile
 180 185 190
 Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg Arg
 195 200 205
 Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Ser Leu Cys Ala Val Leu
 210 215 220
 Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln Glu
 225 230 235 240
 Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp His
 245 250 255
 Leu Glu Ala Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met Glu
 260 265 270
 Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile Asn
 275 280 285
 Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu Pro
 290 295 300
 Gly Tyr Glu Ser Met Glu Gln Phe Thr Val Arg Val Glu His Val Ala
 305 310 315 320
 Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ser Gly Glu Glu
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 Glu Arg Pro Asp Gly Pro
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[illegible]

<400> 59

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tgg cgg ggc cgc tcc ttc gcc ctg gcg cgt gcg gca ggc gcg ccc cac 148
 Trp Arg Gly Arg Ser Phe Ala Leu Ala Arg Ala Ala Gly Ala Pro His
 25 30 35

ggt ggt gac ttg cag ccc ccc gcc tgt ccc gag ccg cgc ggg cgc cag 196
Gly Gly Asp Leu Gln Pro Pro Ala Cys Pro Glu Pro Arg Gly Arg Gln
40 45 50 55

ctc agt ttg tcc gcg gcg gcg gtg gtg gac tct gcg ccc cgc ccc ctg 244
Leu Ser Leu Ser Ala Ala Ala Val Val Asp Ser Ala Pro Arg Pro Leu
60 65 70

cag ccg tac ttg cgc ctc atg cgg ttg gac aag ccc att gga acc tgg 292
Gln Pro Tyr Leu Arg Leu Met Arg Leu Asp Lys Pro Ile Gly Thr Trp
75 80 85

c t t c t g t a t t a c c a t g t a c c t g g a g c a t t g g t t g g c a g c t g a a c c a 340
Leu Leu Tyr Leu Pro Cys Thr Trp Ser Ile Gly Leu Ala Ala Glu Pro

90 95 100

ggt tgt ttt cca gat tgg tac atg ctc tcc ctc ttt ggc act gga gct 388
Gly Cys Phe Pro Asp Trp Tyr Met Leu Ser Leu Phe Gly Thr Gly Ala
105 110 115

att ctg atg cgt gga gca ggc tgt act att aat gac atg tgg gac cag 436
Ile Leu Met Arg Gly Ala Gly Cys Thr Ile Asn Asp Met Trp Asp Gln
120 125 130 135

gac tat gat aaa aag gtt aca aga aca gcc aat cgt cca ata gcc gct 484
Asp Tyr Asp Lys Lys Val Thr Arg Thr Ala Asn Arg Pro Ile Ala Ala
140 145 150

gga gac att tca act ttt cag tcc ttt gtt ttt ctt ggg gga cag cta 532
Gly Asp Ile Ser Thr Phe Gln Ser Phe Val Phe Leu Gly Gly Gln Leu
155 160 165

acc ctg gca ctg ggt gtt ctt ctg tgt cta aat tac tac agt ata gct 580
Thr Leu Ala Leu Gly Val Leu Leu Cys Leu Asn Tyr Tyr Ser Ile Ala

170	175	180	
ctg gga gca gga tcc tta ctt ctt gtc atc acc tac cca cta atg aaa			628
Leu Gly Ala Gly Ser Leu Leu Leu Val Ile Thr Tyr Pro Leu Met Lys			
185	190	195	
aga att tca tac tgg cct caa cta gcc ttg ggc ttg aca ttt aat tgg			676
Arg Ile Ser Tyr Trp Pro Gln Leu Ala Leu Gly Leu Thr Phe Asn Trp			
200	205	210	215
gga gcg tta ctt gga tgg tct gct atc aag ggt tcc tgt gat cca tct			724
Gly Ala Leu Leu Gly Trp Ser Ala Ile Lys Gly Ser Cys Asp Pro Ser			
	220	225	230
gtt tgc ctg cct ctt tat ttt tct gga gtt atg tgg aca cta ata tat			772
Val Cys Leu Pro Leu Tyr Phe Ser Gly Val Met Trp Thr Leu Ile Tyr			
	235	240	245
gac act att tat gcc cat cag gac aaa aga gat gat gtt ttg att ggt			820
Asp Thr Ile Tyr Ala His Gln Asp Lys Arg Asp Asp Val Leu Ile Gly			
	250	255	260
ctt aag tca acg gct ctg cgg ttc gga gaa aat acc aag ccg tgg ctc			868
Leu Lys Ser Thr Ala Leu Arg Phe Gly Glu Asn Thr Lys Pro Trp Leu			
	265	270	275
agc ggc ttc agt gtt gca atg ctg ggg gca ctg agc cta gtg ggt gtg			916
Ser Gly Phe Ser Val Ala Met Leu Gly Ala Leu Ser Leu Val Gly Val			
280	285	290	295
aac agt gga cag act gct ccc tac tac gct gcc ctg ggt gct gta gga			964
Asn Ser Gly Gln Thr Ala Pro Tyr Tyr Ala Ala Leu Gly Ala Val Gly			
	300	305	310
gcc cat ctg act cac cag att tac act cta gac atc cac aga cct gag			1012
Ala His Leu Thr His Gln Ile Tyr Thr Leu Asp Ile His Arg Pro Glu			
	315	320	325
gat tgt tgg aat aaa ttt atc tcc aac cga aca ctg gga cta ata gtt			1060
Asp Cys Trp Asn Lys Phe Ile Ser Asn Arg Thr Leu Gly Leu Ile Val			
	330	335	340
ttt tta ggg att gtc ctt ggg aat ttg tgg aaa gaa aag aag aca gac			1108
Phe Leu Gly Ile Val Leu Gly Asn Leu Trp Lys Glu Lys Lys Thr Asp			
	345	350	355
aaa aca aag aag ggt ata gag aat aaa ata gaa aat taa tgaatgaaat			1157
Lys Thr Lys Lys Gly Ile Glu Asn Lys Ile Glu Asn			
360	365	370	
ttatctagga atttttaaaa catttttttac aaaatataat tagatttgaa tacaaaatct			1217
gatacaatat gttaaagaat taagaacctg aagatgaaga tttagagcat atttacctgg			1277
attttactta tttgctagca aaattccccc ttgtcacaga aaccagggac tcttcaggat			1337
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<211> 371
<212> PRT
<213> Homo sapiens

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Arg Ala Ala Gly Ala Pro His Gly Gly Asp Leu Gln Pro Pro Ala Cys
35 40 45
Pro Glu Pro Arg Gly Arg Gln Leu Ser Leu Ser Ala Ala Ala Val Val
50 55 60
Asp Ser Ala Pro Arg Pro Leu Gln Pro Tyr Leu Arg Leu Met Arg Leu
65 70 75 80
Asp Lys Pro Ile Gly Thr Trp Leu Leu Tyr Leu Pro Cys Thr Trp Ser
85 90 95
Ile Gly Leu Ala Ala Glu Pro Gly Cys Phe Pro Asp Trp Tyr Met Leu
100 105 110
Ser Leu Phe Gly Thr Gly Ala Ile Leu Met Arg Gly Ala Gly Cys Thr
115 120 125
Ile Asn Asp Met Trp Asp Gln Asp Tyr Asp Lys Lys Val Thr Arg Thr
130 135 140
Ala Asn Arg Pro Ile Ala Ala Gly Asp Ile Ser Thr Phe Gln Ser Phe
145 150 155 160
Val Phe Leu Gly Gly Gln Leu Thr Leu Ala Leu Gly Val Leu Leu Cys
165 170 175
Leu Asn Tyr Tyr Ser Ile Ala Leu Gly Ala Gly Ser Leu Leu Leu Val
180 185 190
Ile Thr Tyr Pro Leu Met Lys Arg Ile Ser Tyr Trp Pro Gln Leu Ala
195 200 205
Leu Gly Leu Thr Phe Asn Trp Gly Ala Leu Leu Gly Trp Ser Ala Ile
210 215 220
Lys Gly Ser Cys Asp Pro Ser Val Cys Leu Pro Leu Tyr Phe Ser Gly
225 230 235 240
Val Met Trp Thr Leu Ile Tyr Asp Thr Ile Tyr Ala His Gln Asp Lys
245 250 255
Arg Asp Asp Val Leu Ile Gly Leu Lys Ser Thr Ala Leu Arg Phe Gly
260 265 270
Glu Asn Thr Lys Pro Trp Leu Ser Gly Phe Ser Val Ala Met Leu Gly
275 280 285
Ala Leu Ser Leu Val Gly Val Asn Ser Gly Gln Thr Ala Pro Tyr Tyr
290 295 300
Ala Ala Leu Gly Ala Val Gly Ala His Leu Thr His Gln Ile Tyr Thr
305 310 315 320
Leu Asp Ile His Arg Pro Glu Asp Cys Trp Asn Lys Phe Ile Ser Asn
325 330 335
Arg Thr Leu Gly Leu Ile Val Phe Leu Gly Ile Val Leu Gly Asn Leu

Leu	Ser	Pro	Pro	Pro	Glu	Lys	Arg	Gly	Arg	Lys	Ala	Thr	Ser	Gly	Lys		
		130					135					140					
aag	ggg	ggg	aag	aaa	tcc	aag	gct	gcc	aaa	cca	cgg	acg	tcc	aaa	aag	659	
Lys	Gly	Gly	Lys	Lys	Ser	Lys	Ala	Ala	Lys	Pro	Arg	Thr	Ser	Lys	Lys		
	145					150				155							
tcc	aaa	cca	aag	gac	agc	gat	aaa	gaa	gga	act	tca	aat	tcc	acc	tct	707	
Ser	Lys	Pro	Lys	Asp	Ser	Asp	Lys	Glu	Gly	Thr	Ser	Asn	Ser	Thr	Ser		
160					165					170					175		
gaa	gat	ggg	cca	ggg	gat	gga	ttc	acc	att	ctg	tct	tct	aag	agc	ctt	755	
Glu	Asp	Gly	Pro	Gly	Asp	Gly	Phe	Thr	Ile	Leu	Ser	Ser	Lys	Ser	Leu		
				180					185					190			
gtt	ctg	gga	cag	aag	ctg	tcc	tta	acc	cag	agt	gac	atc	agc	cat	att	803	
Val	Leu	Gly	Gln	Lys	Leu	Ser	Leu	Thr	Gln	Ser	Asp	Ile	Ser	His	Ile		
			195					200					205				
ggc	tcc	atg	aga	gtg	gag	ggc	att	gtc	cac	cca	acc	aca	gcc	gaa	att	851	
Gly	Ser	Met	Arg	Val	Glu	Gly	Ile	Val	His	Pro	Thr	Thr	Ala	Glu	Ile		
		210					215					220					
gac	ctc	aaa	gaa	gat	ata	ggt	aaa	gcc	ttg	gaa	aag	gct	ggg	gga	aaa	899	
Asp	Leu	Lys	Glu	Asp	Ile	Gly	Lys	Ala	Leu	Glu	Lys	Ala	Gly	Gly	Lys		
	225					230					235						
gag	ttc	ttg	gaa	acg	gta	aag	gag	ctt	cgc	aaa	tcc	caa	ggc	cct	ttg	947	
Glu	Phe	Leu	Glu	Thr	Val	Lys	Glu	Leu	Arg	Lys	Ser	Gln	Gly	Pro	Leu		
240					245				250						255		
gaa	gtc	gcc	gaa	gcc	gcc	gtc	agc	caa	tcc	agt	gga	ctc	gca	gcc	aaa	995	
Glu	Val	Ala	Glu	Ala	Ala	Val	Ser	Gln	Ser	Ser	Gly	Leu	Ala	Ala	Lys		
				260					265					270			
ttt	gtc	atc	cac	tgt	cac	atc	cct	cag	tgg	ggc	tcc	gac	aaa	tgt	gaa	1043	
Phe	Val	Ile	His	Cys	His	Ile	Pro	Gln	Trp	Gly	Ser	Asp	Lys	Cys	Glu		
			275					280					285				
gaa	cag	ctt	gaa	gag	acc	atc	aaa	aac	tgc	ctg	tca	gcg	gag	gag	gac	1091	
Glu	Gln	Leu	Glu	Glu	Thr	Ile	Lys	Asn	Cys	Leu	Ser	Ala	Ala	Glu	Asp		
		290					295					300					
aag	aag	cta	aag	tcc	gtc	gag	ttc	cag	cct	ttc	ccc	agc	ggc	aga	aac	1139	
Lys	Lys	Leu	Lys	Ser	Val	Ala	Phe	Pro	Pro	Phe	Pro	Ser	Gly	Arg	Asn		
	305					310					315						
tgc	ttt	ccc	aaa	cag	act	gag	gcc	cag	gtg	acc	ctc	aaa	gcc	atc	tca	1187	
Cys	Phe	Pro	Lys	Gln	Thr	Ala	Ala	Gln	Val	Thr	Leu	Lys	Ala	Ile	Ser		
320					325				330						335		
gcc	cac	ttt	gat	gac	tcg	agc	gag	tcc	tcg	ctg	aag	aac	gtg	tac	ttc	1235	
Ala	His	Phe	Asp	Asp	Ser	Ser	Ala	Ser	Ser	Leu	Lys	Asn	Val	Tyr	Phe		
				340					345					350			
ctg	ctc	ttc	gac	agc	gag	agc	atc	ggc	atc	tac	gtg	cag	gag	atg	gcc	1283	
Leu	Leu	Phe	Asp	Ser	Glu	Ser	Ile	Gly	Ile	Tyr	Val	Gln	Glu	Met	Ala		

355

360

365

aag ctc gac gcc aag tag ccgccgcaact ttccagcagg gatcggagga 1331
Lys Leu Asp Ala Lys
370

cgacccgagt cccaagagtg gggtttttgct ttttaaaagg agagaggagg ggtgatggca 1391
ggggagtgga ggggtggccgg gcaggtcctg ccggcgcagg gagccctctg cccttcacac 1451
tctcctccaa aagagcctcc atctgtaagg aagcaggtct ccgcgagggg tttctttcca 1511
tgtgttttcc tcctgttggt ttagaacttt tttaaaaaaa cagacctcgt tttagattta 1571
tagcattgac ttttacacac attcacacaa gaaaaaaatc ctttcaaat tcttaaattct 1631
tctgttcctc ctttttccaa gggaagaggg caaaaagtgg cctgggctct gttggtgtgc 1691
gtgttccgtg gcggagagaa gaaaatggga aagacatctc 1731

<210> 62
<211> 372
<212> PRT
<213> Homo sapiens

<400> 62
Met Ser Gly Arg Ser Gly Lys Lys Lys Met Ser Lys Leu Ser Arg Ser
1 5 10 15
Ala Arg Ala Gly Val Ile Phe Pro Val Gly Arg Leu Met Arg Tyr Leu
20 25 30
Lys Lys Gly Thr Phe Lys Tyr Arg Ile Ser Val Gly Ala Pro Val Tyr
35 40 45
Met Ala Ala Val Ile Glu Tyr Leu Ala Ala Glu Ile Leu Glu Leu Ala
50 55 60
Gly Asn Ala Ala Arg Asp Asn Lys Lys Ala Arg Ile Ala Pro Arg His
65 70 75 80
Ile Leu Leu Ala Val Ala Asn Asp Glu Glu Leu Asn Gln Leu Leu Lys
85 90 95
Gly Val Thr Ile Ala Ser Gly Gly Val Leu Pro Arg Ile His Pro Glu
100 105 110
Leu Leu Ala Lys Lys Arg Gly Thr Lys Gly Lys Ser Glu Thr Ile Leu
115 120 125
Ser Pro Pro Pro Glu Lys Arg Gly Arg Lys Ala Thr Ser Gly Lys Lys
130 135 140
Gly Gly Lys Lys Ser Lys Ala Ala Lys Pro Arg Thr Ser Lys Lys Ser
145 150 155 160
Lys Pro Lys Asp Ser Asp Lys Glu Gly Thr Ser Asn Ser Thr Ser Glu
165 170 175
Asp Gly Pro Gly Asp Gly Phe Thr Ile Leu Ser Ser Lys Ser Leu Val
180 185 190
Leu Gly Gln Lys Leu Ser Leu Thr Gln Ser Asp Ile Ser His Ile Gly
195 200 205
Ser Met Arg Val Glu Gly Ile Val His Pro Thr Thr Ala Glu Ile Asp
210 215 220
Leu Lys Glu Asp Ile Gly Lys Ala Leu Glu Lys Ala Gly Gly Lys Glu
225 230 235 240

Phe Leu Glu Thr Val Lys Glu Leu Arg Lys Ser Gln Gly Pro Leu Glu
 245 250 255
 Val Ala Glu Ala Ala Val Ser Gln Ser Ser Gly Leu Ala Ala Lys Phe
 260 265 270
 Val Ile His Cys His Ile Pro Gln Trp Gly Ser Asp Lys Cys Glu Glu
 275 280 285
 Gln Leu Glu Glu Thr Ile Lys Asn Cys Leu Ser Ala Ala Glu Asp Lys
 290 295 300
 Lys Leu Lys Ser Val Ala Phe Pro Pro Phe Pro Ser Gly Arg Asn Cys
 305 310 315 320
 Phe Pro Lys Gln Thr Ala Ala Gln Val Thr Leu Lys Ala Ile Ser Ala
 325 330 335
 His Phe Asp Asp Ser Ser Ala Ser Ser Leu Lys Asn Val Tyr Phe Leu
 340 345 350
 Leu Phe Asp Ser Glu Ser Ile Gly Ile Tyr Val Gln Glu Met Ala Lys
 355 360 365
 Leu Asp Ala Lys
 370

<210> 63
 <211> 910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (21)..(698)

<400> 63
 aaagtaaggg tgtcgtgctg atg gcc ctg tgc gca ctg acc cgc gct ctg cgc 53
 Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Arg
 1 5 10

tct ctg aac ctg gcg ccc ccg acc gtc gcc gcc cct gcc ccg agt ctg 101
 Ser Leu Asn Leu Ala Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu
 15 20 25

ttc ccc gcc gcc cag atg atg aac aat ggc ctc ctc caa cag ccc tct 149
 Phe Pro Ala Ala Gln Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser
 30 35 40

gcc ttg atg ttg ctc ccc tgc cgc cca gtt ctt act tct gtg gcc ctt 197
 Ala Leu Met Leu Leu Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu
 45 50 55

aat gcc aac ttt gtg tcc tgg aag agt cgt acc aag tac acc att aca 245
 Asn Ala Asn Phe Val Ser Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr
 60 65 70 75

cca gtg aag atg agg aag tct ggg ggc cga gac cac aca ggc cga atc 293
 Pro Val Lys Met Arg Lys Ser Gly Gly Arg Asp His Thr Gly Arg Ile
 80 85 90

cgg gtg cat ggt att ggc ggg ggc cac aag caa cgt tat cga atg att 341
 Arg Val His Gly Ile Gly Gly Gly His Lys Gln Arg Tyr Arg Met Ile

95	100	105	
gac ttt ctg cgt ttc cgg cct gag gag acc aag tca gga ccc ttt gag			389
Asp Phe Leu Arg Phe Arg Pro Glu Glu Thr Lys Ser Gly Pro Phe Glu			
110	115	120	
gag aag gtt atc caa gtc cgc tat gat ccc tgt agg tca gca gac ata			437
Glu Lys Val Ile Gln Val Arg Tyr Asp Pro Cys Arg Ser Ala Asp Ile			
125	130	135	
gct ctg gtt gct ggg ggc agc cgg aaa cgc tgg atc atc gcc aca gaa			485
Ala Leu Val Ala Gly Gly Ser Arg Lys Arg Trp Ile Ile Ala Thr Glu			
140	145	150	155
aac atg cag gct gga gat aca atc ttg aac tct aac cac ata ggc cga			533
Asn Met Gln Ala Gly Asp Thr Ile Leu Asn Ser Asn His Ile Gly Arg			
160	165	170	
atg gca gtt gct gct cgg gaa ggg gat gcg cat cct ctt ggg gct ctg			581
Met Ala Val Ala Ala Arg Glu Gly Asp Ala His Pro Leu Gly Ala Leu			
175	180	185	
cct gtg ggg acc ctc atc aac aac gtg gaa agt gag cca ggc cgg ggt			629
Pro Val Gly Thr Leu Ile Asn Asn Val Glu Ser Glu Pro Gly Arg Gly			
190	195	200	
gcc caa tat atc cga gct gca ggt gct gga aac gtg cgt agc aac agt			677
Ala Gln Tyr Ile Arg Ala Ala Gly Ala Gly Asn Val Arg Ser Asn Ser			
205	210	215	
agg ccg agt atc caa cgt tga tcataacaaa cgggtcattg gcaaggcagg			728
Arg Pro Ser Ile Gln Arg			
220	225		
tcgcaaccgc tggctgggca agaggcctaa cagtgggcgg tggcaccgca aggggggctg			788
ggctggccga aagattcggc cactaccccc catgaagagt tacgtgaagc tgccttctgc			848
ttctgcccga agctgatata cctgtactct aataaaatgc cccccccccc cgttttaatc			908
tg			910

<210> 64
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Arg Ser Leu Asn Leu Ala
 1 5 10 15
 Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln
 20 25 30
 Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu
 35 40 45
 Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val
 50 55 60

<400> 67
agaagacagg gcacccgcgg ccttgctgcg catgctcgcg ctgtgacccc ggcttgaggt 60
aacagcgcgga gctgaggctg gggcccttgg cgcggaggct gagggaccgg ccgcggcgct 120
gtcgccggag agggagggca ccgctgtcgc cagaagccaa ggagtcctca gtgaccgtgg 180
gatccacaac atctccacat cgctgtcccc acccagccag ggcagcgcca gcactagctc 240
agacgcaagg acggaaccgc tggactccag gttccttgcc tgggagtagg agaaatccac 300
ctgtgggggg ctgagtgtgg cctgagggac aggccctggg tcccggg atg ccc ctg 356
Met Pro Leu
1
ccc gag ccc agc gag cag gag ggt gag agt gtg aag gcc agc cag gag 404
Pro Glu Pro Ser Glu Gln Glu Gly Glu Ser Val Lys Ala Ser Gln Glu
5 10 15
cca tcc ccc aag cca ggc aca gaa gtc atc ccg gca gcc ccc agg aag 452
Pro Ser Pro Lys Pro Gly Thr Glu Val Ile Pro Ala Ala Pro Arg Lys
20 25 30 35
ccc aga aag ttc tcc aaa ctg gtc ctg ctc aca gcc tcc aaa gac agc 500
Pro Arg Lys Phe Ser Lys Leu Val Leu Leu Thr Ala Ser Lys Asp Ser
40 45 50
acc aag gtg gcg ggg gcc aag cgc aag ggt gtg cac tgt gtc atg tcc 548
Thr Lys Val Ala Gly Ala Lys Arg Lys Gly Val His Cys Val Met Ser
55 60 65
ctg ggg gtg ccc ggc ccc gcc acc ctt gcc aag gcc ctc ctc cag acc 596
Leu Gly Val Pro Gly Pro Ala Thr Leu Ala Lys Ala Leu Leu Gln Thr
70 75 80
cac ccc gag gcc cag cgg gcc att gag gca gcc cct cag gag cct gag 644
His Pro Glu Ala Gln Arg Ala Ile Glu Ala Ala Pro Gln Glu Pro Glu
85 90 95
cag aaa cgg agc agg cag gac cca ggc aca gac aga aca gaa gac agt 692
Gln Lys Arg Ser Arg Gln Asp Pro Gly Thr Asp Arg Thr Glu Asp Ser
100 105 110 115
gga tta gca gcg ggg cct cct gag gct gct ggg gag aac ttt gcc ccc 740
Gly Leu Ala Ala Gly Pro Pro Glu Ala Ala Gly Glu Asn Phe Ala Pro
120 125 130
tgc tct gtg gcg ccc ggc aag tcc ctg taa ccttgacaac aggcgcaccc 790
Cys Ser Val Ala Pro Gly Lys Ser Leu
135 140
tcccggggcca ccaaccagc cataggctct tctctgtccg cagggttct ggggccaaat 850
gggtgaatct ttgctttcaa cattgtgtga tttcttttct tttttttttt ttttttttag 910
atcaagtata agttactttt gtaagcagaa aaatactttc aaacaagaat aaaagaagct 970

gttcgctaga cccc

984

<210> 68
<211> 140
<212> PRT
<213> Homo sapiens

<400> 68
Met Pro Leu Pro Glu Pro Ser Glu Gln Glu Gly Glu Ser Val Lys Ala
1 5 10 15
Ser Gln Glu Pro Ser Pro Lys Pro Gly Thr Glu Val Ile Pro Ala Ala
20 25 30
Pro Arg Lys Pro Arg Lys Phe Ser Lys Leu Val Leu Leu Thr Ala Ser
35 40 45
Lys Asp Ser Thr Lys Val Ala Gly Ala Lys Arg Lys Gly Val His Cys
50 55 60
Val Met Ser Leu Gly Val Pro Gly Pro Ala Thr Leu Ala Lys Ala Leu
65 70 75 80
Leu Gln Thr His Pro Glu Ala Gln Arg Ala Ile Glu Ala Ala Pro Gln
85 90 95
Glu Pro Glu Gln Lys Arg Ser Arg Gln Asp Pro Gly Thr Asp Arg Thr
100 105 110
Glu Asp Ser Gly Leu Ala Ala Gly Pro Pro Glu Ala Ala Gly Glu Asn
115 120 125
Phe Ala Pro Cys Ser Val Ala Pro Gly Lys Ser Leu
130 135 140

<210> 69
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (357)..(614)

<400> 69
gtatgatgga agtcgtagta ggaaatggcg tcgtggcatt gaggggcata cctcctagaa 60
cctccaggaa aagctcgcg aagacgaggt tctgcggaga gagaggctcc aagcagtctg 120
ggaagtgtag tccagttggc ttagcagtag tttcgttggg ggggagccga ggttccggga 180
aggggctagg ccggcttgaa aagagattat gactgtacct tttactttg tagctggaac 240
acaagaagtg tttgtttaat gaatgacgta cacatttaag atctgtttgg acgcgaggga 300
taatcctgtg aattgctaag agttcactgg gtttggccct tagtggtgac ttcagt atg 359
Met
1

ctg aga cgg aaa cca aca cgc cta gag cta aag ctt gat gac att gaa 407
Leu Arg Arg Lys Pro Thr Arg Leu Glu Leu Lys Leu Asp Asp Ile Glu

<220>
 <221> CDS
 <222> (121)..(1860)

<400> 71

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aggcctgcgg agggggcggtta tctggagggc cgcgggtgca ggccgcagtg acagggccgc 60

tcgccccgct agtctcgctt gtctcccggg gcagctgtgt tcgcggcctg caggcccaac 120

atg gcg cag gag gtg tcg gag tac ctg agc cag aac ccg cgg gtg gca 168
Met Ala Gln Glu Val Ser Glu Tyr Leu Ser Gln Asn Pro Arg Val Ala
  1             5             10             15

gcc tgg gtg gag gcg ctg cgc tgc gac ggc gag act gac aaa cac tgg 216
Ala Trp Val Glu Ala Leu Arg Cys Asp Gly Glu Thr Asp Lys His Trp
             20             25             30

cgc cac cgc cgg gat ttt ttg ctt cgc aac gcc ggg gac ctg gcc ccc 264
Arg His Arg Arg Asp Phe Leu Leu Arg Asn Ala Gly Asp Leu Ala Pro
             35             40             45

gct ggc ggc gct gcc tcc gct agc acg gat gaa gct gcc gac gcc gag 312
Ala Gly Gly Ala Ala Ser Ala Ser Thr Asp Glu Ala Ala Asp Ala Glu
             50             55             60

agc ggg acc cga aac cgg cag ctg cag cag ctc atc tcc ttt tcc atg 360
Ser Gly Thr Arg Asn Arg Gln Leu Gln Gln Leu Ile Ser Phe Ser Met
             65             70             75             80

gcc tgg gcg aac cac gtc ttc ctc ggg tgc cga tac cct caa aaa gtt 408
Ala Trp Ala Asn His Val Phe Leu Gly Cys Arg Tyr Pro Gln Lys Val
             85             90             95

atg gat aaa ata ctt agt atg gct gaa ggc atc aaa gtg aca gat gct 456
Met Asp Lys Ile Leu Ser Met Ala Glu Gly Ile Lys Val Thr Asp Ala
             100            105            110

cca acc tat aca aca aga gat gaa ctg gtt gcc aag gtg aag aaa aga 504
Pro Thr Tyr Thr Thr Arg Asp Glu Leu Val Ala Lys Val Lys Lys Arg
             115            120            125

ggg ata tcg agt agc aat gaa ggg gta gaa gag cca tcc aaa aaa cga 552
Gly Ile Ser Ser Ser Asn Glu Gly Val Glu Glu Pro Ser Lys Lys Arg
             130            135            140

gtt ata gaa gga aaa aac agt tct gca gtt gag caa gat cac gca aaa 600
Val Ile Glu Gly Lys Asn Ser Ser Ala Val Glu Gln Asp His Ala Lys
             145            150            155            160

acc tct gcc aag aca gaa cgt gca tca gct cag cag gaa aac agt tca 648
Thr Ser Ala Lys Thr Glu Arg Ala Ser Ala Gln Gln Glu Asn Ser Ser
             165            170            175

acg tgt ata ggg tcg gcc atc aaa tca gag agt ggg aac tca gct cgg 696
Thr Cys Ile Gly Ser Ala Ile Lys Ser Glu Ser Gly Asn Ser Ala Arg
             180            185            190

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agc tct ggc atc tcc agt cag aat agc tct aca agt gat gga gat cga	744
Ser Ser Gly Ile Ser Ser Gln Asn Ser Ser Thr Ser Asp Gly Asp Arg	
195 200 205	
tct gtt tcc agc caa agc agc agc agc gtt tcc tct cag gta aca acg	792
Ser Val Ser Ser Gln Ser Ser Ser Ser Val Ser Ser Gln Val Thr Thr	
210 215 220	
gca gga tct ggg aaa gct tct gaa gca gaa gct cca gat aaa cac ggt	840
Ala Gly Ser Gly Lys Ala Ser Glu Ala Glu Ala Pro Asp Lys His Gly	
225 230 235 240	
tca tca ttt gtt tcc ttg ctg aaa tcc agt gtg aat agt cac atg acc	888
Ser Ser Phe Val Ser Leu Leu Lys Ser Ser Val Asn Ser His Met Thr	
245 250 255	
caa tcc act gat tct aga caa caa agt gga tca cct aaa aag agt gct	936
Gln Ser Thr Asp Ser Arg Gln Gln Ser Gly Ser Pro Lys Lys Ser Ala	
260 265 270	
ttg gaa ggc tct tca gcc tca gct tct cga agc agc tca gag atc gag	984
Leu Glu Gly Ser Ser Ala Ser Ala Ser Arg Ser Ser Ser Glu Ile Glu	
275 280 285	
gtg ccc ttg ttg ggc tcc tca gga agc tca gag gta gaa ttg cca cta	1032
Val Pro Leu Leu Gly Ser Ser Gly Ser Ser Glu Val Glu Leu Pro Leu	
290 295 300	
ttg tct tcc aaa cct agt tca gag aca gct tca agt ggg tta act tcc	1080
Leu Ser Ser Lys Pro Ser Ser Glu Thr Ala Ser Ser Gly Leu Thr Ser	
305 310 315 320	
aaa act agt tca gag gca agt gtt tca tca tca gtt gct aaa aac agt	1128
Lys Thr Ser Ser Glu Ala Ser Val Ser Ser Ser Val Ala Lys Asn Ser	
325 330 335	
tcc tca tca ggc aca tcc tta ctg act ccc aag agc agc tct tca aca	1176
Ser Ser Ser Gly Thr Ser Leu Leu Thr Pro Lys Ser Ser Ser Ser Thr	
340 345 350	
aat aca tcg ctg cta act tcc aag agc act tcc cag gta gct gca tca	1224
Asn Thr Ser Leu Leu Thr Ser Lys Ser Thr Ser Gln Val Ala Ala Ser	
355 360 365	
cta cta gct tcc aag agc agc tcc cag acc agt gga tct ctg gtt tcc	1272
Leu Leu Ala Ser Lys Ser Ser Ser Gln Thr Ser Gly Ser Leu Val Ser	
370 375 380	
aaa agc act tcc tta gca agt gtg tcc cag ttg gct tct aag agt agt	1320
Lys Ser Thr Ser Leu Ala Ser Val Ser Gln Leu Ala Ser Lys Ser Ser	
385 390 395 400	
tct cag act agc acc tca cag ttg cct tct aaa agt act tca cag tca	1368
Ser Gln Thr Ser Thr Ser Gln Leu Pro Ser Lys Ser Thr Ser Gln Ser	
405 410 415	
agt gag agt tct gtc aaa ttc tct tgc aag tta acc aat gaa gat gtg	1416

Ser	Glu	Ser	Ser	Val	Lys	Phe	Ser	Cys	Lys	Leu	Thr	Asn	Glu	Asp	Val		
			420					425					430				
aaa	cag	aag	caa	cct	ttt	ttc	aat	aga	cta	tat	aaa	acg	gtg	gca	tgg	1464	
Lys	Gln	Lys	Gln	Pro	Phe	Phe	Asn	Arg	Leu	Tyr	Lys	Thr	Val	Ala	Trp		
		435					440					445					
aag	ttg	gta	gct	gtt	ggc	ttt	agt	ccc	aat	gtg	aat	cat	gga	gag		1512	
Lys	Leu	Val	Ala	Val	Gly	Gly	Phe	Ser	Pro	Asn	Val	Asn	His	Gly	Glu		
		450				455					460						
ctc	cta	aat	gca	gct	att	gag	gct	ctg	aaa	gca	aca	ctg	gat	gta	ttt	1560	
Leu	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Leu	Lys	Ala	Thr	Leu	Asp	Val	Phe		
465					470					475					480		
ttt	gtc	cca	cta	aaa	gaa	ttg	gca	gat	ctg	cct	caa	aat	aag	agc	tct	1608	
Phe	Val	Pro	Leu	Lys	Glu	Leu	Ala	Asp	Leu	Pro	Gln	Asn	Lys	Ser	Ser		
				485					490					495			
caa	gaa	agt	att	gtt	tgt	gaa	ttg	agg	tgc	aag	tct	gtg	tat	ttg	ggc	1656	
Gln	Glu	Ser	Ile	Val	Cys	Glu	Leu	Arg	Cys	Lys	Ser	Val	Tyr	Leu	Gly		
			500					505					510				
act	ggc	tgt	gga	aaa	agc	aaa	gaa	aat	gca	aaa	gca	gtt	gca	tca	aga	1704	
Thr	Gly	Cys	Gly	Lys	Ser	Lys	Glu	Asn	Ala	Lys	Ala	Val	Ala	Ser	Arg		
		515					520					525					
gaa	gca	ttg	aag	tta	ttt	ctc	aag	aaa	aag	gtg	gtg	gta	aaa	ata	tgt	1752	
Glu	Ala	Leu	Lys	Leu	Phe	Leu	Lys	Lys	Lys	Val	Val	Val	Lys	Ile	Cys		
		530				535					540						
aaa	agg	aaa	tac	aga	ggc	agt	gaa	ata	gaa	gat	cta	gta	ctc	ctt	gat	1800	
Lys	Arg	Lys	Tyr	Arg	Gly	Ser	Glu	Ile	Glu	Asp	Leu	Val	Leu	Leu	Asp		
545					550					555					560		
gaa	gaa	tcg	agg	cct	gta	aac	tta	cct	cca	gca	cta	aaa	cat	cct	caa	1848	
Glu	Glu	Ser	Arg	Pro	Val	Asn	Leu	Pro	Pro	Ala	Leu	Lys	His	Pro	Gln		
				565					570					575			
gaa	tta	cta	taa	tgtgtccaaa	atatcactgc	atacaatatc	tggtatttga									1900	
Glu	Leu	Leu															
agagaaaaac	tgactttt	gt	atagtataaa	acacaggc	tt	tcacaaat	tt	tgtattg	c	tt						1960	
tttttccagt	tttgcagaaa	atttacattc	tagttctctt	cacacagtag	cagttg	taaa										2020	
taatttatga	atgacagtac	acattaaaag	gtatgcatta	gcagcatatt	agtatg	ctgt										2080	
tttatttgct	gaagaaaata	ctgtcttcta	tttttaatga	tacattaggt	acgatgtg	ta										2140	
gttcggtaga	gtcctaaaa	ttttgtacta	ctttcaattt	ggtgaaaatg	tattaagt	ttg										2200	
tctaccatgt	tttcttttct	agctgaataa	accacatcaa	aggaaaggga	ccacagtatt											2260	
tgaatgtttg	aaagtctgta	aagcttaagg	ttttaaaaa	gttgcccgt	atgttgaacg											2320	
tgtctgttaa	aaaataaaag	aaaaaatagt	tgcttcaa	ac	tatttttatg	agaagt	ttgta									2380	

agcatttttt agatataaag cagtataaag tacttggttat tttactctga agttgttttaa 2440
aattcaccat gactttgacc gctgaagatt ctttaagcgg gttaatttat gttttgaggt 2500
ggaatacaat ttacactttt ttcttaaaaa catgaatgtg ggtttctata ttaagcatat 2560
tttgtgacta ctattaacag attgatttgt ttagatatta aatgctttaa gctattt 2617

<210> 72
<211> 579
<212> PRT
<213> Homo sapiens

<400> 72
Met Ala Gln Glu Val Ser Glu Tyr Leu Ser Gln Asn Pro Arg Val Ala
1 5 10 15
Ala Trp Val Glu Ala Leu Arg Cys Asp Gly Glu Thr Asp Lys His Trp
20 25 30
Arg His Arg Arg Asp Phe Leu Leu Arg Asn Ala Gly Asp Leu Ala Pro
35 40 45
Ala Gly Gly Ala Ala Ser Ala Ser Thr Asp Glu Ala Ala Asp Ala Glu
50 55 60
Ser Gly Thr Arg Asn Arg Gln Leu Gln Gln Leu Ile Ser Phe Ser Met
65 70 75 80
Ala Trp Ala Asn His Val Phe Leu Gly Cys Arg Tyr Pro Gln Lys Val
85 90 95
Met Asp Lys Ile Leu Ser Met Ala Glu Gly Ile Lys Val Thr Asp Ala
100 105 110
Pro Thr Tyr Thr Thr Arg Asp Glu Leu Val Ala Lys Val Lys Lys Arg
115 120 125
Gly Ile Ser Ser Ser Asn Glu Gly Val Glu Glu Pro Ser Lys Lys Arg
130 135 140
Val Ile Glu Gly Lys Asn Ser Ser Ala Val Glu Gln Asp His Ala Lys
145 150 155 160
Thr Ser Ala Lys Thr Glu Arg Ala Ser Ala Gln Gln Glu Asn Ser Ser
165 170 175
Thr Cys Ile Gly Ser Ala Ile Lys Ser Glu Ser Gly Asn Ser Ala Arg
180 185 190
Ser Ser Gly Ile Ser Ser Gln Asn Ser Ser Thr Ser Asp Gly Asp Arg
195 200 205
Ser Val Ser Ser Gln Ser Ser Ser Ser Val Ser Ser Gln Val Thr Thr
210 215 220
Ala Gly Ser Gly Lys Ala Ser Glu Ala Glu Ala Pro Asp Lys His Gly
225 230 235 240
Ser Ser Phe Val Ser Leu Leu Lys Ser Ser Val Asn Ser His Met Thr
245 250 255
Gln Ser Thr Asp Ser Arg Gln Gln Ser Gly Ser Pro Lys Lys Ser Ala
260 265 270
Leu Glu Gly Ser Ser Ala Ser Ala Ser Arg Ser Ser Ser Glu Ile Glu
275 280 285
Val Pro Leu Leu Gly Ser Ser Gly Ser Ser Glu Val Glu Leu Pro Leu
290 295 300
Leu Ser Ser Lys Pro Ser Ser Glu Thr Ala Ser Ser Gly Leu Thr Ser
305 310 315 320
Lys Thr Ser Ser Glu Ala Ser Val Ser Ser Ser Val Ala Lys Asn Ser

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          325          330          335
Ser Ser Ser Gly Thr Ser Leu Leu Thr Pro Lys Ser Ser Ser Ser Thr
          340          345          350
Asn Thr Ser Leu Leu Thr Ser Lys Ser Thr Ser Gln Val Ala Ala Ser
          355          360          365
Leu Leu Ala Ser Lys Ser Ser Ser Gln Thr Ser Gly Ser Leu Val Ser
          370          375          380
Lys Ser Thr Ser Leu Ala Ser Val Ser Gln Leu Ala Ser Lys Ser Ser
385          390          395          400
Ser Gln Thr Ser Thr Ser Gln Leu Pro Ser Lys Ser Thr Ser Gln Ser
          405          410          415
Ser Glu Ser Ser Val Lys Phe Ser Cys Lys Leu Thr Asn Glu Asp Val
          420          425          430
Lys Gln Lys Gln Pro Phe Phe Asn Arg Leu Tyr Lys Thr Val Ala Trp
          435          440          445
Lys Leu Val Ala Val Gly Gly Phe Ser Pro Asn Val Asn His Gly Glu
          450          455          460
Leu Leu Asn Ala Ala Ile Glu Ala Leu Lys Ala Thr Leu Asp Val Phe
465          470          475          480
Phe Val Pro Leu Lys Glu Leu Ala Asp Leu Pro Gln Asn Lys Ser Ser
          485          490          495
Gln Glu Ser Ile Val Cys Glu Leu Arg Cys Lys Ser Val Tyr Leu Gly
          500          505          510
Thr Gly Cys Gly Lys Ser Lys Glu Asn Ala Lys Ala Val Ala Ser Arg
          515          520          525
Glu Ala Leu Lys Leu Phe Leu Lys Lys Lys Val Val Val Lys Ile Cys
          530          535          540
Lys Arg Lys Tyr Arg Gly Ser Glu Ile Glu Asp Leu Val Leu Leu Asp
545          550          555          560
Glu Glu Ser Arg Pro Val Asn Leu Pro Pro Ala Leu Lys His Pro Gln
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Glu Leu Leu

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<210> 73
 <211> 1810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (39)..(1121)

<400> 73
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cgc agc cga cgg ctg gga ggc cta agg ccc gaa tcc ccc gag agc ctc 104
 Arg Ser Arg Arg Leu Gly Gly Leu Arg Pro Glu Ser Pro Glu Ser Leu
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acc tca gtt tcg cgg acg aga cgg gcc ctt gtg gag ttc gag tcg aac 152
 Thr Ser Val Ser Arg Thr Arg Arg Ala Leu Val Glu Phe Glu Ser Asn
 25 30 35

cca gaa gaa acg agg gag ccc ggg tct cct ccg agt gtg cag cgg gct	200
Pro Glu Glu Thr Arg Glu Pro Gly Ser Pro Pro Ser Val Gln Arg Ala	
40 45 50	
ggc ctg ggg tcc ccc gaa agg ccg ccg aag aca agc cca gga tca ccc	248
Gly Leu Gly Ser Pro Glu Arg Pro Pro Lys Thr Ser Pro Gly Ser Pro	
55 60 65 70	
cgt ctg cag cag ggt gca ggc ttg gag tca ccc caa ggg cag cca gag	296
Arg Leu Gln Gln Gly Ala Gly Leu Glu Ser Pro Gln Gly Gln Pro Glu	
75 80 85	
cca ggc gca gcg tcc ccc cag cgt cag caa gac cta cac ctg gag tcg	344
Pro Gly Ala Ala Ser Pro Gln Arg Gln Gln Asp Leu His Leu Glu Ser	
90 95 100	
cct caa aga cag cca gag tac agt cct gaa tcc cca cga tgt cag ccg	392
Pro Gln Arg Gln Pro Glu Tyr Ser Pro Glu Ser Pro Arg Cys Gln Pro	
105 110 115	
aag cca agt gag gag gca cca aag tgt tct cag gac cag gga gta ctg	440
Lys Pro Ser Glu Glu Ala Pro Lys Cys Ser Gln Asp Gln Gly Val Leu	
120 125 130	
gcc tcg gag ttg gcc cag aat aag gag gag ctg acc ccg ggg gcc ccc	488
Ala Ser Glu Leu Ala Gln Asn Lys Glu Glu Leu Thr Pro Gly Ala Pro	
135 140 145 150	
cag cat cag cta ccg ccg gtc cca gga tca cca gag cct tac ccc ggt	536
Gln His Gln Leu Pro Pro Val Pro Gly Ser Pro Glu Pro Tyr Pro Gly	
155 160 165	
cag caa gct ccc ggt ccg gag ccc tct cag cca cta ctg gag ctg aca	584
Gln Gln Ala Pro Gly Pro Glu Pro Ser Gln Pro Leu Leu Glu Leu Thr	
170 175 180	
ccc agg gca cct ggc tcc ccc ccg ggt cag cat gag ccg agc aag cca	632
Pro Arg Ala Pro Gly Ser Pro Arg Gly Gln His Glu Pro Ser Lys Pro	
185 190 195	
cct cca gct ggg gag acg gtg aca ggc ggc ttc ggg gca aag aag cga	680
Pro Pro Ala Gly Glu Thr Val Thr Gly Gly Phe Gly Ala Lys Lys Arg	
200 205 210	
aaa ggt tct tca tcc cag gcc cca gcg tcc aag aag ttg aat aaa gag	728
Lys Gly Ser Ser Ser Gln Ala Pro Ala Ser Lys Lys Leu Asn Lys Glu	
215 220 225 230	
gag ctt cct gta atc ccg aag ggg aag ccc aaa tcg ggg cga gtg tgg	776
Glu Leu Pro Val Ile Pro Lys Gly Lys Pro Lys Ser Gly Arg Val Trp	
235 240 245	
aag gac cgc tcc aag aaa aga ttc tcc cag atg ctt cag gac aag ccc	824
Lys Asp Arg Ser Lys Lys Arg Phe Ser Gln Met Leu Gln Asp Lys Pro	
250 255 260	
ctg cgc aca tcg tgg cag ccg aag atg aag gaa cga cag gag agg aag	872

Leu Arg Thr Ser Trp Gln Arg Lys Met Lys Glu Arg Gln Glu Arg Lys
 265 270 275
 ctg gcc aag gac ttt gcc cgt cac ctg gag gag gag aag gag agg cgc 920
 Leu Ala Lys Asp Phe Ala Arg His Leu Glu Glu Glu Lys Glu Arg Arg
 280 285 290
 cgc cag gag aag aaa cag cgc cgg gct gag aac ctg aaa cgc cgc ctg 968
 Arg Gln Glu Lys Lys Gln Arg Arg Ala Glu Asn Leu Lys Arg Arg Leu
 295 300 305 310
 gag aat gag cgg aag gca gag gtc gtc caa gtg atc cga aac ccc gcc 1016
 Glu Asn Glu Arg Lys Ala Glu Val Val Gln Val Ile Arg Asn Pro Ala
 315 320 325
 aag ctc aag cgg gca aag aag aag cag ctg cgc tcc att gag aag cgg 1064
 Lys Leu Lys Arg Ala Lys Lys Lys Gln Leu Arg Ser Ile Glu Lys Arg
 330 335 340
 gac acc ctg gcc ctg ctg cag aag cag ccg ccc cag cag ccg gca gcc 1112
 Asp Thr Leu Ala Leu Leu Gln Lys Gln Pro Pro Gln Gln Pro Ala Ala
 345 350 355
 aag atc tga gctcaggacg gcccagggcc ttccatggcc aacaacctg 1161
 Lys Ile
 360
 tcagacacag cacctcaggc cgctgctcag atgcctctgc tggagctggc actccaaacc 1221
 catggctcca gaacagggac cccaccccg accggggctc ctcagccttt gaaggcttcc 1281
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 aggttgacag gagcagagct tttccctagc acccactttc ccaaaccagt ctctgcagaa 1701
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 gttgcataca ggcacaatcc taggcactgg caaatacaga caatagacc 1810
 <210> 74
 <211> 360
 <212> PRT
 <213> Homo sapiens
 <400> 74
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Glu	Ser	Pro	Glu	Ser	Leu	Thr
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Val	Glu	Phe	Glu	Ser	Asn	Pro
35				40		45
Pro	Ser	Val	Gln	Arg	Ala	Gly
50				55		60
Thr	Ser	Pro	Gly	Ser	Pro	Arg
65				70		75
Pro	Gln	Gly	Gln	Pro	Glu	Pro
85				90		95
Asp	Leu	His	Leu	Glu	Ser	Pro
100				105		110
Ser	Pro	Arg	Cys	Gln	Pro	Lys
115				120		125
Gln	Asp	Gln	Gly	Val	Leu	Ala
130				135		140
Leu	Thr	Pro	Gly	Ala	Pro	Gln
145				150		155
Pro	Glu	Pro	Tyr	Pro	Gly	Gln
165				170		175
Pro	Leu	Leu	Glu	Leu	Thr	Pro
180				185		190
His	Glu	Pro	Ser	Lys	Pro	Pro
195				200		205
Phe	Gly	Ala	Lys	Lys	Arg	Lys
210				215		220
Lys	Lys	Leu	Asn	Lys	Glu	Glu
225				230		235
Lys	Ser	Gly	Arg	Val	Trp	Lys
245				250		255
Met	Leu	Gln	Asp	Lys	Pro	Leu
260				265		270
Glu	Arg	Gln	Glu	Arg	Lys	Leu
275				280		285
Glu	Glu	Lys	Glu	Arg	Arg	Arg
290				295		300
Asn	Leu	Lys	Arg	Arg	Leu	Glu
305				310		315
Val	Ile	Arg	Asn	Pro	Ala	Lys
325				330		335
Arg	Ser	Ile	Glu	Lys	Arg	Asp
340				345		350
Pro	Gln	Gln	Pro	Ala	Ala	Lys
355				360		

<210> 75
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (217)..(597)

<400> 75

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acggaagcta cagtgagaac atagccagtc ccaaagacaa tttcaaagaa aaatgacagt 1277
aaagattagc tgggagtagt ctttgacagt gcttatttga tactgtctct cagagtttgc 1337
aaaccagatt gtacaagtca ttagcgtcag atagctttaa agttgtgacc ttcttgatga 1397
tgaatcttct agccagtttc ctttcctttg taacgaaaca tgaaatccta gaatgtatga 1457
gaagttcaga cattagggcat aaggaaactc gtttgcaggc tctctgtcca gggctgcttc 1517
ctgtcctgga ggggccagtg agtcttaggt atgtttatct tattctcaca tttgtgtttt 1577
tttagaaaag tgaatggtca ataaatggct tatctttcat aat 1620

<210> 76
<211> 126
<212> PRT
<213> Homo sapiens

<400> 76
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Gly Thr Ser Gln Ala Ser Ala Gly Ala Ala Thr Gly Ala Thr Gly Ala
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Ser Gly Gly Gly Gly Pro Ile Asn Pro Ala Ser Leu Pro Pro Gly Asp
35 40 45
Pro Gln Leu Ile Ala Leu Ile Val Glu Gln Leu Lys Ser Arg Gly Leu
50 55 60
Phe Asp Ser Phe Arg Arg Asp Cys Leu Ala Asp Val Asp Thr Lys Pro
65 70 75 80
Ala Tyr Gln Asn Leu Arg Gln Lys Val Asp Asn Phe Val Ser Thr His
85 90 95
Leu Asp Lys Gln Glu Trp Asn Pro Thr Met Asn Lys Asn Gln Leu Arg
100 105 110
Asn Gly Leu Arg Gln Ser Val Val Gln Leu Gly Asp Cys Gly
115 120 125

<210> 77
<211> 1349
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (185)..(1042)

<400> 77
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cggcacgtcc gcgaggactt gaagtcctga gcgctcaagt ttgtccgtag gtcgagagaa 180

ggcc atg gag gtg ccg cca ccg gca ccg cgg agc ttt ctc tgt aga gca 229
Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala
1 5 10 15

ttg tgc cta ttt ccc cga gtc ttt gct gcc gaa gct gtg act gcc gat 277
Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp
20 25 30

tcg gaa gtc ctt gag gag cgt cag aag cgg ctt ccc tac gtc cca gag 325
Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu
35 40 45

ccc tat tac ccg gaa tct gga tgg gac cgc ctc cgg gag ctg ttt ggc 373
Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly
50 55 60

aaa gat gaa cag cag aga att tca aag gac ctt gct aat atc tgt aag 421
Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala Asn Ile Cys Lys
65 70 75

acg gca gct aca gca ggc atc att ggc tgg gtg tat ggg gga ata cca 469
Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val Tyr Gly Gly Ile Pro
80 85 90 95

gct ttt att cat gct aaa caa caa tac att gag cag agc cag gca gaa 517
Ala Phe Ile His Ala Lys Gln Gln Tyr Ile Glu Gln Ser Gln Ala Glu
100 105 110

att tat cat aac cgg ttt gat gct gtg caa tct gca cat cgt gct gcc 565
Ile Tyr His Asn Arg Phe Asp Ala Val Gln Ser Ala His Arg Ala Ala
115 120 125

aca cga ggc ttc att cgt tat ggc tgg cgc tgg ggt tgg aga act gca 613
Thr Arg Gly Phe Ile Arg Tyr Gly Trp Arg Trp Gly Trp Arg Thr Ala
130 135 140

gtg ttt gtg act ata ttc aac aca gtg aac act agt ctg aat gta tac 661
Val Phe Val Thr Ile Phe Asn Thr Val Asn Thr Ser Leu Asn Val Tyr
145 150 155

cga aat aaa gat gcc tta agc cat ttt gta att gca gga gct gtc acg 709
Arg Asn Lys Asp Ala Leu Ser His Phe Val Ile Ala Gly Ala Val Thr
160 165 170 175

gga agt ctt ttt agg ata aac gta ggc ctg cgt ggc ctg gtg gct ggt 757
Gly Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly
180 185 190

ggc ata att gga gcc ttg ctg ggc act cct gta gga ggc ctg ctg atg 805
Gly Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met
195 200 205

gca ttt cag aag tac tct ggt gag act gtt cag gaa aga aaa cag aag 853

145		150		155		160
Asn Lys Asp Ala Leu Ser His Phe Val Ile Ala Gly Ala Val Thr Gly						
	165		170		175	
Ser Leu Phe Arg Ile Asn Val Gly Leu Arg Gly Leu Val Ala Gly Gly						
	180		185		190	
Ile Ile Gly Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala						
	195		200		205	
Phe Gln Lys Tyr Ser Gly Glu Thr Val Gln Glu Arg Lys Gln Lys Asp						
	210		215		220	
Arg Lys Ala Leu His Glu Leu Lys Leu Glu Glu Trp Lys Gly Arg Leu						
225		230		235		240
Gln Val Thr Glu His Leu Pro Glu Lys Ile Glu Ser Ser Leu Gln Glu						
	245		250		255	
Asp Glu Pro Glu Asn Asp Ala Lys Lys Ile Glu Ala Leu Leu Asn Leu						
	260		265		270	
Pro Arg Asn Pro Ser Val Ile Asp Lys Gln Asp Lys Asp						
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<210> 79
 <211> 1355
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (79)..(1068)

<400> 79
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cgaagccaca caggagcc atg gaa gtg gca gag ccc agc agc ccc act gaa 111
 Met Glu Val Ala Glu Pro Ser Ser Pro Thr Glu
 1 5 10

gag gag gag gag gaa gag gag cac tcg gca gag cct cgg ccc cgc act 159
 Glu Glu Glu Glu Glu Glu Glu His Ser Ala Glu Pro Arg Pro Arg Thr
 15 20 25

cgc tcc aat cct gaa ggg gct gag gac cgg gca gta ggg gca cag gcc 207
 Arg Ser Asn Pro Glu Gly Ala Glu Asp Arg Ala Val Gly Ala Gln Ala
 30 35 40

agc gtg ggc agc cgc agc gag ggt gag ggt gag gcc gcc agt gct gat 255
 Ser Val Gly Ser Arg Ser Glu Gly Glu Gly Glu Ala Ala Ser Ala Asp
 45 50 55

gat ggg agc ctc aac act tca gga gcc ggc cct aag tcc tgg cag gtg 303
 Asp Gly Ser Leu Asn Thr Ser Gly Ala Gly Pro Lys Ser Trp Gln Val
 60 65 70 75

ccc ccg cca gcc cct gag gtc caa att cgg aca cca agg gtc aac tgt 351
 Pro Pro Pro Ala Pro Glu Val Gln Ile Arg Thr Pro Arg Val Asn Cys
 80 85 90

cca gag aaa gtg att atc tgc ctg gac ctg tca gag gaa atg tca ctg 399

Pro	Glu	Lys	Val	Ile	Ile	Cys	Leu	Asp	Leu	Ser	Glu	Glu	Met	Ser	Leu		
			95					100					105				
cca	aag	ctg	gag	tcg	ttc	aac	ggc	tcc	aaa	acc	aac	gcc	ctc	aat	gtc	447	
Pro	Lys	Leu	Glu	Ser	Phe	Asn	Gly	Ser	Lys	Thr	Asn	Ala	Leu	Asn	Val		
		110					115					120					
tcc	cag	aag	atg	att	gag	atg	ttc	gtg	cgg	aca	aaa	cac	aag	atc	gac	495	
Ser	Gln	Lys	Met	Ile	Glu	Met	Phe	Val	Arg	Thr	Lys	His	Lys	Ile	Asp		
		125					130				135						
aaa	agc	cac	gag	ttt	gca	ctg	gtg	gtg	gtg	aac	gat	gac	acg	gcc	tgg	543	
Lys	Ser	His	Glu	Phe	Ala	Leu	Val	Val	Val	Asn	Asp	Asp	Thr	Ala	Trp		
140					145					150					155		
ctg	tct	ggc	ctg	acc	tcc	gac	ccc	cgc	gag	ctc	tgt	agc	tgc	ctc	tat	591	
Leu	Ser	Gly	Leu	Thr	Ser	Asp	Pro	Arg	Glu	Leu	Cys	Ser	Cys	Leu	Tyr		
				160					165					170			
gat	ctg	gag	acg	gcc	tcc	tgt	tcc	acc	ttc	aat	ctg	gaa	gga	ctt	ttc	639	
Asp	Leu	Glu	Thr	Ala	Ser	Cys	Ser	Thr	Phe	Asn	Leu	Glu	Gly	Leu	Phe		
			175					180					185				
agc	ctc	atc	cag	cag	aaa	act	gag	ctt	ccg	gtc	aca	gag	aac	gtg	cag	687	
Ser	Leu	Ile	Gln	Gln	Lys	Thr	Glu	Leu	Pro	Val	Thr	Glu	Asn	Val	Gln		
		190					195					200					
acg	att	ccc	ccg	cca	tat	gtg	gtc	cgc	acc	atc	ctt	gtc	tac	agc	cgt	735	
Thr	Ile	Pro	Pro	Pro	Tyr	Val	Val	Arg	Thr	Ile	Leu	Val	Tyr	Ser	Arg		
	205					210					215						
cca	cct	tgc	cag	ccc	cag	ttc	tcc	ttg	acg	gag	ccc	atg	aag	aaa	atg	783	
Pro	Pro	Cys	Gln	Pro	Gln	Phe	Ser	Leu	Thr	Glu	Pro	Met	Lys	Lys	Met		
220					225					230					235		
ttc	cag	tgc	cca	tat	ttc	ttc	ttt	gac	gtt	gtt	tac	atc	cac	aat	ggc	831	
Phe	Gln	Cys	Pro	Tyr	Phe	Phe	Phe	Asp	Val	Val	Tyr	Ile	His	Asn	Gly		
				240				245						250			
act	gag	gag	aag	gag	gag	gag	atg	agt	tgg	aag	gat	atg	ttt	gcc	ttc	879	
Thr	Glu	Glu	Lys	Glu	Glu	Glu	Met	Ser	Trp	Lys	Asp	Met	Phe	Ala	Phe		
			255				260						265				
atg	ggc	agc	ctg	gat	acc	aag	ggc	acc	agc	tac	aaa	tat	gag	gtg	gca	927	
Met	Gly	Ser	Leu	Asp	Thr	Lys	Gly	Thr	Ser	Tyr	Lys	Tyr	Glu	Val	Ala		
		270					275					280					
ctg	gct	ggg	cca	gcc	ctg	gag	ttg	cac	aac	tgc	atg	gcg	aaa	ctg	ttg	975	
Leu	Ala	Gly	Pro	Ala	Leu	Glu	Leu	His	Asn	Cys	Met	Ala	Lys	Leu	Leu		
		285				290					295						
gcc	cac	ccc	ctg	cag	cgg	cct	tgc	cag	agc	cat	gct	tcc	tac	agc	ctg	1023	
Ala	His	Pro	Leu	Gln	Arg	Pro	Cys	Gln	Ser	His	Ala	Ser	Tyr	Ser	Leu		
300					305					310					315		
ctg	gag	gag	gag	gat	gaa	gcc	att	gag	gtt	gag	gcc	act	gtc	tga		1068	
Leu	Glu	Glu	Glu	Asp	Glu	Ala	Ile	Glu	Val	Glu	Ala	Thr	Val				

320

325

accatccctg tacatctgca ccttcttgtg caaggaagtc cttggcctaa agccttggtt 1128
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 cttgcagggt cctaggaggg aaaccaggga ttccaggagg gatcccagga actgtgggca 1248
 cccattttct gtgtctccca gccatttcc actcctagtt tgtcatggat aatttttgtt 1308
 cttccctgtg tgatttttgc catcaaaata aaaatttgag actcgtt 1355

<210> 80

<211> 329

<212> PRT

<213> Homo sapiens

<400> 80

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 Gly Ala Glu Asp Arg Ala Val Gly Ala Gln Ala Ser Val Gly Ser Arg
 35 40 45
 Ser Glu Gly Glu Gly Glu Ala Ala Ser Ala Asp Asp Gly Ser Leu Asn
 50 55 60
 Thr Ser Gly Ala Gly Pro Lys Ser Trp Gln Val Pro Pro Pro Ala Pro
 65 70 75 80
 Glu Val Gln Ile Arg Thr Pro Arg Val Asn Cys Pro Glu Lys Val Ile
 85 90 95
 Ile Cys Leu Asp Leu Ser Glu Glu Met Ser Leu Pro Lys Leu Glu Ser
 100 105 110
 Phe Asn Gly Ser Lys Thr Asn Ala Leu Asn Val Ser Gln Lys Met Ile
 115 120 125
 Glu Met Phe Val Arg Thr Lys His Lys Ile Asp Lys Ser His Glu Phe
 130 135 140
 Ala Leu Val Val Val Asn Asp Asp Thr Ala Trp Leu Ser Gly Leu Thr
 145 150 155 160
 Ser Asp Pro Arg Glu Leu Cys Ser Cys Leu Tyr Asp Leu Glu Thr Ala
 165 170 175
 Ser Cys Ser Thr Phe Asn Leu Glu Gly Leu Phe Ser Leu Ile Gln Gln
 180 185 190
 Lys Thr Glu Leu Pro Val Thr Glu Asn Val Gln Thr Ile Pro Pro Pro
 195 200 205
 Tyr Val Val Arg Thr Ile Leu Val Tyr Ser Arg Pro Pro Cys Gln Pro
 210 215 220
 Gln Phe Ser Leu Thr Glu Pro Met Lys Lys Met Phe Gln Cys Pro Tyr
 225 230 235 240
 Phe Phe Phe Asp Val Val Tyr Ile His Asn Gly Thr Glu Glu Lys Glu
 245 250 255
 Glu Glu Met Ser Trp Lys Asp Met Phe Ala Phe Met Gly Ser Leu Asp
 260 265 270
 Thr Lys Gly Thr Ser Tyr Lys Tyr Glu Val Ala Leu Ala Gly Pro Ala
 275 280 285
 Leu Glu Leu His Asn Cys Met Ala Lys Leu Leu Ala His Pro Leu Gln
 290 295 300

T04269.92906950

Arg Pro Cys Gln Ser His Ala Ser Tyr Ser Leu Leu Glu Glu Glu Asp
 305 310 315 320
 Glu Ala Ile Glu Val Glu Ala Thr Val
 325

<210> 81
 <211> 1543
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (29)..(730)

<400> 81
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 Cys Ser Arg Gly Cys Ala Gly Gly Cys Glu Cys Gly Asp Lys Gly Lys
 10 15 20

tgc agc gac tcc tcg ctg ttg ggc aag aga ctc tcc gaa gac tcg agc 148
 Cys Ser Asp Ser Ser Leu Leu Gly Lys Arg Leu Ser Glu Asp Ser Ser
 25 30 35 40

cgc cac cag ctg ttg cag aag tgg gcg agc atg tgg agc tcc atg agc 196
 Arg His Gln Leu Leu Gln Lys Trp Ala Ser Met Trp Ser Ser Met Ser
 45 50 55

gaa gac gcg tcg gtg gcc gac atg gag agg gcg cag ctg gag gag gag 244
 Glu Asp Ala Ser Val Ala Asp Met Glu Arg Ala Gln Leu Glu Glu Glu
 60 65 70

gcg gcg gct gcg gag gag agg ccg ctg gtg ttc ctg tgc tcc ggc tgc 292
 Ala Ala Ala Ala Glu Glu Arg Pro Leu Val Phe Leu Cys Ser Gly Cys
 75 80 85

cgg cgg ccg ctg ggc gac tcg ctg agc tgg gtg gcc agc cag gag gac 340
 Arg Arg Pro Leu Gly Asp Ser Leu Ser Trp Val Ala Ser Gln Glu Asp
 90 95 100

acc aac tgc atc ctg ctt cgc tgt gtt tcc tgt aat gtt tct gtg gat 388
 Thr Asn Cys Ile Leu Leu Arg Cys Val Ser Cys Asn Val Ser Val Asp
 105 110 115 120

aag gaa cag aag cta tcc aaa cgt gaa aag gaa aat ggt tgc gtc ctt 436
 Lys Glu Gln Lys Leu Ser Lys Arg Glu Lys Glu Asn Gly Cys Val Leu
 125 130 135

gag act ttg tgc tgc gcg ggg tgc tca ctc aat ctt ggc tac gtg tac 484
 Glu Thr Leu Cys Cys Ala Gly Cys Ser Leu Asn Leu Gly Tyr Val Tyr
 140 145 150

1	5	10	15
Cys Glu Cys Gly Asp Lys Gly Lys Cys Ser Asp Ser Ser Leu Leu Gly			
	20	25	30
Lys Arg Leu Ser Glu Asp Ser Ser Arg His Gln Leu Leu Gln Lys Trp			
	35	40	45
Ala Ser Met Trp Ser Ser Met Ser Glu Asp Ala Ser Val Ala Asp Met			
	50	55	60
Glu Arg Ala Gln Leu Glu Glu Glu Ala Ala Ala Glu Glu Arg Pro			
	65	70	75
Leu Val Phe Leu Cys Ser Gly Cys Arg Arg Pro Leu Gly Asp Ser Leu			
	85	90	95
Ser Trp Val Ala Ser Gln Glu Asp Thr Asn Cys Ile Leu Leu Arg Cys			
	100	105	110
Val Ser Cys Asn Val Ser Val Asp Lys Glu Gln Lys Leu Ser Lys Arg			
	115	120	125
Glu Lys Glu Asn Gly Cys Val Leu Glu Thr Leu Cys Cys Ala Gly Cys			
	130	135	140
Ser Leu Asn Leu Gly Tyr Val Tyr Arg Cys Thr Pro Lys Asn Leu Asp			
	145	150	155
Tyr Lys Arg Asp Leu Phe Cys Leu Ser Val Glu Ala Ile Glu Ser Tyr			
	165	170	175
Val Leu Gly Ser Ser Glu Lys Gln Ile Val Ser Glu Asp Lys Glu Leu			
	180	185	190
Phe Asn Leu Glu Ser Arg Val Glu Ile Glu Lys Ser Leu Thr Gln Met			
	195	200	205
Glu Asp Val Leu Lys Ala Leu Gln Met Lys Leu Trp Glu Ala Glu Ser			
	210	215	220
Lys Leu Ser Phe Ala Thr Cys Lys Ser			
225	230		

<210> 83
 <211> 1436
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (31)..(582)

<400> 83
 acgtgaccca agccccagct tcgcgcaggg atg gag ccg gaa gag ggg acg ccc 54
 Met Glu Pro Glu Glu Gly Thr Pro
 1 5

ttg tgg cgg ctg cag aag ctg ccg gcc gag ctg ggc ccg cag ctt ctt 102
 Leu Trp Arg Leu Gln Lys Leu Pro Ala Glu Leu Gly Pro Gln Leu Leu
 10 15 20

cac aaa ata att gat ggc att tgt ggt cga gct tat cct gtg tac caa 150
 His Lys Ile Ile Asp Gly Ile Cys Gly Arg Ala Tyr Pro Val Tyr Gln
 25 30 35 40

gat tat cac act gtt tgg gaa tca gaa gaa tgg atg cac gtt tta gaa 198
 Asp Tyr His Thr Val Trp Glu Ser Glu Glu Trp Met His Val Leu Glu
 45 50 55

gat att gcc aaa ttt ttc aaa gcc ata gtt ggt aaa aac tta cct gat	246
Asp Ile Ala Lys Phe Phe Lys Ala Ile Val Gly Lys Asn Leu Pro Asp	
60 65 70	
gaa gag ata ttt cag cag ttg aat cag ttg aat tca ctt cat caa gaa	294
Glu Glu Ile Phe Gln Gln Leu Asn Gln Leu Asn Ser Leu His Gln Glu	
75 80 85	
act atc atg aaa tgc gtg aaa agt agg aaa gat gaa atc aaa cag gct	342
Thr Ile Met Lys Cys Val Lys Ser Arg Lys Asp Glu Ile Lys Gln Ala	
90 95 100	
ctg tca aga gaa ata gtt gct att tcc tct gca cag cta cag gat ttt	390
Leu Ser Arg Glu Ile Val Ala Ile Ser Ser Ala Gln Leu Gln Asp Phe	
105 110 115 120	
gat tgg cag gta aag ctt gca ctt tcc agt gac aag att gct gca tta	438
Asp Trp Gln Val Lys Leu Ala Leu Ser Ser Asp Lys Ile Ala Ala Leu	
125 130 135	
cga atg cca ctt tta agc ctg cat cta gat gta aaa gaa aat ggt gaa	486
Arg Met Pro Leu Leu Ser Leu His Leu Asp Val Lys Glu Asn Gly Glu	
140 145 150	
gta aaa cct tat tct att gaa atg agt aga gag gag ctg cag aat cta	534
Val Lys Pro Tyr Ser Ile Glu Met Ser Arg Glu Glu Leu Gln Asn Leu	
155 160 165	
ata cag tcc ttg gaa gca gcg aat aag gtg gtc ctg cag ttg aaa taa	582
Ile Gln Ser Leu Glu Ala Ala Asn Lys Val Val Leu Gln Leu Lys	
170 175 180	
ctggaaatga tgaataccag tcctatcaga ttttattgct ccaacttata tggcagagtg	642
aatactgcgt gttcagaaac cttgtgatgt cttgactgtt gcaccaggct gagaaagcag	702
caatattgat attataaaga taaaaattta tcaacattcc ttaacaggaa attacatggt	762
tgagaggaaa tgcataaaat gaaagatgaa aaatctatag tagcagttta tattttcatg	822
attgttttgc ctcatattatt aaatatttga gaaatctttg gagatacata gttttattga	882
aagctaaaaa taggttctaa agtaatgtaa aaatataaag cacaaatata cttgaatatt	942
gcttaaagaa ttgtgtgaat agcaacatat attatggata tatactttgt gatattttta	1002
aaaaataatt ttttcaaaga atgtataagc tgcataatata actcaggaga ttccatgtct	1062
ttctcatatt tcagaggaaa gattataaaa tataaaattt cttagagaac acctctttgt	1122
cagagataaa caagaacaaa tactctaaac ttatgtgaac agttttgagt ttatgaattc	1182
tagaaactaa aatcaagaat acagaaaaat gaaaataaca ttttacttct gcgcttctat	1242
gtttgggaaa cattgctctg ataaaaaata gctgtcatta tgcagtgtgt atattcaa	1302
atgagataag actatgtaca catccacttt tgtaataaaa ctcaatattg aatacttttg	1362

gatgttaaatt tcattggaaa aacaaacccat ttgtaacctc agttaacttt aacaacaagc 1422

attctgagca aatg 1436

<210> 84
<211> 183
<212> PRT
<213> Homo sapiens

<400> 84
Met Glu Pro Glu Gly Thr Pro Leu Trp Arg Leu Gln Lys Leu Pro
1 5 10 15
Ala Glu Leu Gly Pro Gln Leu Leu His Lys Ile Ile Asp Gly Ile Cys
20 25 30
Gly Arg Ala Tyr Pro Val Tyr Gln Asp Tyr His Thr Val Trp Glu Ser
35 40 45
Glu Glu Trp Met His Val Leu Glu Asp Ile Ala Lys Phe Phe Lys Ala
50 55 60
Ile Val Gly Lys Asn Leu Pro Asp Glu Glu Ile Phe Gln Gln Leu Asn
65 70 75 80
Gln Leu Asn Ser Leu His Gln Glu Thr Ile Met Lys Cys Val Lys Ser
85 90 95
Arg Lys Asp Glu Ile Lys Gln Ala Leu Ser Arg Glu Ile Val Ala Ile
100 105 110
Ser Ser Ala Gln Leu Gln Asp Phe Asp Trp Gln Val Lys Leu Ala Leu
115 120 125
Ser Ser Asp Lys Ile Ala Ala Leu Arg Met Pro Leu Leu Ser Leu His
130 135 140
Leu Asp Val Lys Glu Asn Gly Glu Val Lys Pro Tyr Ser Ile Glu Met
145 150 155 160
Ser Arg Glu Glu Leu Gln Asn Leu Ile Gln Ser Leu Glu Ala Ala Asn
165 170 175
Lys Val Val Leu Gln Leu Lys
180

<210> 85
<211> 1357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (102)..(1244)

<400> 85
ggtttccggc gagagggcca gagtgagtgt ttacaccggc ggcagtgcgg ccgggttcct 60
tccgcgggac ggggagaaag agagagcgcg aaagagagag g atg tct ctc tca gac 116
Met Ser Leu Ser Asp
1 5

tgg cac ctg gcg gtg aag ctg gct gac cag cca ctt act cca aag tct 164
Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro Leu Thr Pro Lys Ser
10 15 20

att ctt cgg ttg cca gag aca gaa ctg gga gaa tac tcg cta ggg ggc	212
Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu Tyr Ser Leu Gly Gly	
25 30 35	
tat agt att tca ttt ctg aag cag ctt att gct ggc aaa ctc cag gag	260
Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala Gly Lys Leu Gln Glu	
40 45 50	
tct gtt cca gac cct gag ctg att gat ctg atc tac tgt ggt cgg aag	308
Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile Tyr Cys Gly Arg Lys	
55 60 65	
cta aaa gat gac cag aca ctt gac ttc tat ggc att caa cct ggg tcc	356
Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly Ser	
70 75 80 85	
act gtc cat gtt ctg cga aag tcc tgg cct gaa cct gat cag aaa ccg	404
Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys Pro	
90 95 100	
gaa cct gtg gac aaa gtg gct gcc atg aga gag ttc cgg gtg ttg cac	452
Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu His	
105 110 115	
act gcc ctg cac agc agc tcc tct tac agg gag gcg gtc ttt aag atg	500
Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys Met	
120 125 130	
ctc agc aat aag gag tct ctg gat cag atc att gtg gcc acc cca ggc	548
Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro Gly	
135 140 145	
ctc agc agt gac cct att gct ctt ggg gtt ctc cag gac aag gac ctc	596
Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp Leu	
150 155 160 165	
ttc tct gtc ttc gct gat ccc aat atg ctt gat acg ttg gtg cct gct	644
Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro Ala	
170 175 180	
cac cca gcc ctc gtc aat gcc att gtc ctg gtt ctg cac tcc gta gca	692
His Pro Ala Leu Val Asn Ala Ile Val Leu Val Leu His Ser Val Ala	
185 190 195	
ggc agt gcc cca atg cct ggg act gac tcc tct tcc cgg agc atg ccc	740
Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser Ser Arg Ser Met Pro	
200 205 210	
tcc agc tca tac cgg gat atg cca ggt ggc ttc ctg ttt gaa ggg ctc	788
Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe Leu Phe Glu Gly Leu	
215 220 225	
tca gat gat gag gat gac ttt cac cca aac acc agg tcc aca ccc tct	836
Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr Arg Ser Thr Pro Ser	
230 235 240 245	

agc agt act ccc agc tcc cgc cca gcc tcc ctg ggg tac agt gga gct 884
 Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly Ala
 250 255 260

gct ggg ccc cgg ccc atc acc cag agt gag ctg gcc acc gcc ttg gcc 932
 Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu Ala
 265 270 275

ctg gcc agc act ccg gag agc agc tct cac aca ccg act cct ggc acc 980
 Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly Thr
 280 285 290

cag ggt cat tcc tca ggg acc tca cca atg tcc tct ggt gtc cag tca 1028
 Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser Ser Gly Val Gln Ser
 295 300 305

ggg acg ccc atc acc aat gat ctc ttc agc caa gcc cta cag cat gcc 1076
 Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His Ala
 310 315 320 325

ctt cag gcc tct ggg cag ccc agc ctt cag agc cag tgg cag ccc cag 1124
 Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro Gln
 330 335 340

ctg cag cag cta cgt gac atg ggc atc cag gac gat gag ctg agc ctg 1172
 Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser Leu
 345 350 355

cgg gcc ctg cag gcc acc ggt ggg gac atc caa gca gcc ctg gag ctc 1220
 Arg Ala Leu Gln Ala Thr Gly Gly Asp Ile Gln Ala Ala Leu Glu Leu
 360 365 370

atc ttt gct gga gga gcc cca tga actccctgct tcccctgaac cccagcaag 1274
 Ile Phe Ala Gly Gly Ala Pro
 375 380

ttgcagaggc tactgccctt gggaggcact catgaaggtg cctccatctc tcccttcccc 1334

aatatacctg atggtcaact ctc 1357

<210> 86
 <211> 380
 <212> PRT
 <213> Homo sapiens

<400> 86
 Met Ser Leu Ser Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro
 1 5 10 15
 Leu Thr Pro Lys Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu
 20 25 30
 Tyr Ser Leu Gly Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala
 35 40 45
 Gly Lys Leu Gln Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile
 50 55 60
 Tyr Cys Gly Arg Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly
 65 70 75 80

Ile	Gln	Pro	Gly	Ser	Thr	Val	His	Val	Leu	Arg	Lys	Ser	Trp	Pro	Glu
				85					90					95	
Pro	Asp	Gln	Lys	Pro	Glu	Pro	Val	Asp	Lys	Val	Ala	Ala	Met	Arg	Glu
			100					105					110		
Phe	Arg	Val	Leu	His	Thr	Ala	Leu	His	Ser	Ser	Ser	Ser	Tyr	Arg	Glu
			115				120						125		
Ala	Val	Phe	Lys	Met	Leu	Ser	Asn	Lys	Glu	Ser	Leu	Asp	Gln	Ile	Ile
			130				135				140				
Val	Ala	Thr	Pro	Gly	Leu	Ser	Ser	Asp	Pro	Ile	Ala	Leu	Gly	Val	Leu
145					150					155					160
Gln	Asp	Lys	Asp	Leu	Phe	Ser	Val	Phe	Ala	Asp	Pro	Asn	Met	Leu	Asp
				165					170					175	
Thr	Leu	Val	Pro	Ala	His	Pro	Ala	Leu	Val	Asn	Ala	Ile	Val	Leu	Val
			180					185					190		
Leu	His	Ser	Val	Ala	Gly	Ser	Ala	Pro	Met	Pro	Gly	Thr	Asp	Ser	Ser
			195				200					205			
Ser	Arg	Ser	Met	Pro	Ser	Ser	Ser	Tyr	Arg	Asp	Met	Pro	Gly	Gly	Phe
			210				215				220				
Leu	Phe	Glu	Gly	Leu	Ser	Asp	Asp	Glu	Asp	Asp	Phe	His	Pro	Asn	Thr
225					230					235					240
Arg	Ser	Thr	Pro	Ser	Ser	Ser	Thr	Pro	Ser	Ser	Arg	Pro	Ala	Ser	Leu
				245					250					255	
Gly	Tyr	Ser	Gly	Ala	Ala	Gly	Pro	Arg	Pro	Ile	Thr	Gln	Ser	Glu	Leu
			260					265					270		
Ala	Thr	Ala	Leu	Ala	Leu	Ala	Ser	Thr	Pro	Glu	Ser	Ser	Ser	His	Thr
			275				280					285			
Pro	Thr	Pro	Gly	Thr	Gln	Gly	His	Ser	Ser	Gly	Thr	Ser	Pro	Met	Ser
			290				295				300				
Ser	Gly	Val	Gln	Ser	Gly	Thr	Pro	Ile	Thr	Asn	Asp	Leu	Phe	Ser	Gln
305					310					315					320
Ala	Leu	Gln	His	Ala	Leu	Gln	Ala	Ser	Gly	Gln	Pro	Ser	Leu	Gln	Ser
				325					330					335	
Gln	Trp	Gln	Pro	Gln	Leu	Gln	Gln	Leu	Arg	Asp	Met	Gly	Ile	Gln	Asp
			340					345					350		
Asp	Glu	Leu	Ser	Leu	Arg	Ala	Leu	Gln	Ala	Thr	Gly	Gly	Asp	Ile	Gln
			355				360					365			
Ala	Ala	Leu	Glu	Leu	Ile	Phe	Ala	Gly	Gly	Ala	Pro				
			370			375					380				

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<210> 87
<211> 1399
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (74)..(856)
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<400> 87
 aaaaagcgga cccgcggacg gtggcgtaa gggaacgctg aggtcccgcg cccccgacc 60

gaggttatatc tcc atg aat aac cta aat gat ccc cca aat tgg aat atc 109
Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile
1 5 10

cgg cct aat tcc agg gcg gat ggt ggt gat gga agc agg tgg aat tat	157
Arg Pro Asn Ser Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr	
15 20 25	
gcc ctg ttg gtt cca atg ctg gga ttg gct gct ttt cgt tgg att tgg	205
Ala Leu Leu Val Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp	
30 35 40	
tct agg gag tcc cag aaa gaa gta gaa aaa gag aga gaa gcc tac cgt	253
Ser Arg Glu Ser Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg	
45 50 55 60	
cgg aga act gct gct ttt caa cag gat ctg gaa gcc aag tac cac gcc	301
Arg Arg Thr Ala Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala	
65 70 75	
atg atc tca gaa aat cgg cgt gct gtc gct cag ttg tcc ttg gaa ctc	349
Met Ile Ser Glu Asn Arg Arg Ala Val Ala Gln Leu Ser Leu Glu Leu	
80 85 90	
gaa aag gaa caa aac aga act gct agt tac cga gaa gcc ctt atc tct	397
Glu Lys Glu Gln Asn Arg Thr Ala Ser Tyr Arg Glu Ala Leu Ile Ser	
95 100 105	
cag gga cgc aag ttg gta gaa gaa aag aag ctt ctg gaa cag gaa cgg	445
Gln Gly Arg Lys Leu Val Glu Glu Lys Lys Leu Leu Glu Gln Glu Arg	
110 115 120	
gcc cag gtg atg caa gaa aaa aga cag gtg cag cct ttg aga agt gcg	493
Ala Gln Val Met Gln Glu Lys Arg Gln Val Gln Pro Leu Arg Ser Ala	
125 130 135 140	
tat ttg agc tgc ctg caa agg gaa gaa aac tgg caa agg aga gcc agg	541
Tyr Leu Ser Cys Leu Gln Arg Glu Glu Asn Trp Gln Arg Arg Ala Arg	
145 150 155	
ctt ttg ctg aaa gaa ttt gaa gct gtt ctc aca gaa aga cag aat atc	589
Leu Leu Leu Lys Glu Phe Glu Ala Val Leu Thr Glu Arg Gln Asn Ile	
160 165 170	
tac tgc agt ctg ttt ctt cct cgc agc aag cgg ctg gag ata gag aag	637
Tyr Cys Ser Leu Phe Leu Pro Arg Ser Lys Arg Leu Glu Ile Glu Lys	
175 180 185	
agc tta ctg gtg cga gcg tcc gtc gac ccc gtc gcc gct gac cta gag	685
Ser Leu Leu Val Arg Ala Ser Val Asp Pro Val Ala Ala Asp Leu Glu	
190 195 200	
atg gca gcc ggt ctc acc gac ata ttt cag cat gat aca tac tgt ggt	733
Met Ala Ala Gly Leu Thr Asp Ile Phe Gln His Asp Thr Tyr Cys Gly	
205 210 215 220	
gat gtc tgg aac acc aac aaa cgc cag aat ggc aga ctc atg tgg ctc	781
Asp Val Trp Asn Thr Asn Lys Arg Gln Asn Gly Arg Leu Met Trp Leu	
225 230 235	
tat ctc aaa tac tgg gaa ctc gtt gtc gaa ctg aag aag ttt aag aga	829

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Tyr Leu Lys Tyr Trp Glu Leu Val Val Glu Leu Lys Lys Phe Lys Arg
240 245 250

gta gag gaa gcc ata cta gaa aag taa gacaagagtg aaatcaaact 876
Val Glu Glu Ala Ile Leu Glu Lys
255 260

gcttttagtg actcgaggcc aggcagtcac gcgccttctg ggtctccggc gtcttccggt 936
cccgtgctgc ccgtgtcatg gccacaccgt cacccttcag cagcgacctc cactcccgcc 996
accgtctgag cagaagtgc ccgaagcctc agagacagag ggtctcctcc cgatgctctg 1056
ccgctgttgg ggatatgggt tcttgaagca ttttaggct gccagtattg tattaagcag 1116
aacagtataa cctcgtatatt tagctccagg gtaaaaatgg ttttttaaaa agtcaaatac 1176
aatactggtc cttagcacia gtaattttct gtctgtttca tcaactcccta aatactttct 1236
cctcaaatta tttttctctg tcaccagatt acattaagaa tttgtcagat aatgtgtaga 1296
actgcataac aggtaataga aagtagtaat attatattat caagggttta tatttttaaag 1356
atctctctca ctccataaag gggaaatacc aagtgtttct tgt 1399

<210> 88
<211> 260
<212> PRT
<213> Homo sapiens

<400> 88
Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg Pro Asn Ser
1 5 10 15
Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala Leu Leu Val
20 25 30
Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser Arg Glu Ser
35 40 45
Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg Arg Thr Ala
50 55 60
Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met Ile Ser Glu
65 70 75 80
Asn Arg Arg Ala Val Ala Gln Leu Ser Leu Glu Leu Glu Lys Glu Gln
85 90 95
Asn Arg Thr Ala Ser Tyr Arg Glu Ala Leu Ile Ser Gln Gly Arg Lys
100 105 110
Leu Val Glu Glu Lys Lys Leu Leu Glu Gln Glu Arg Ala Gln Val Met
115 120 125
Gln Glu Lys Arg Gln Val Gln Pro Leu Arg Ser Ala Tyr Leu Ser Cys
130 135 140
Leu Gln Arg Glu Glu Asn Trp Gln Arg Arg Ala Arg Leu Leu Leu Lys
145 150 155 160
Glu Phe Glu Ala Val Leu Thr Glu Arg Gln Asn Ile Tyr Cys Ser Leu
165 170 175
Phe Leu Pro Arg Ser Lys Arg Leu Glu Ile Glu Lys Ser Leu Leu Val
180 185 190
Arg Ala Ser Val Asp Pro Val Ala Ala Asp Leu Glu Met Ala Ala Gly

	195		200		205	
Leu Thr Asp Ile Phe Gln His Asp Thr Tyr Cys Gly Asp Val Trp Asn						
210		215		220		
Thr Asn Lys Arg Gln Asn Gly Arg Leu Met Trp Leu Tyr Leu Lys Tyr						
225		230		235		240
Trp Glu Leu Val Val Glu Leu Lys Lys Phe Lys Arg Val Glu Glu Ala						
	245		250			255
Ile Leu Glu Lys						
260						

<210> 89
 <211> 1119
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (152)..(976)

<400> 89
 ttagctgctc aagctggaga actgtcttcc ttcccagctt cctccgtgtc tgggggtgggg 60
 gatggggggg tctcaggcag ggatactcta gcccttgac tgctgtttag accctgctgt 120
 agctgctgct gctccctgcc cagccccagc c atg aaa ctg ccc aag ggg acc 172
 Met Lys Leu Pro Lys Gly Thr
 1 5
 agg agc tct gtg tac ttt gca cag cac cca gaa aag gag cca ttg ccc 220
 Arg Ser Ser Val Tyr Phe Ala Gln His Pro Glu Lys Glu Pro Leu Pro
 10 15 20
 tca agg cag gag gtc aag cag acc cct gtc atc atg gcc aag atc aaa 268
 Ser Arg Gln Glu Val Lys Gln Thr Pro Val Ile Met Ala Lys Ile Lys
 25 30 35
 ggt ccg ggg ccc gcc aag tac ctc cgg cca tcc tgc acg ggc tac ata 316
 Gly Pro Gly Pro Ala Lys Tyr Leu Arg Pro Ser Cys Thr Gly Tyr Ile
 40 45 50 55
 gat cat gac atc tcc atg ttc aag gca cca gct tat acc ctg cat agc 364
 Asp His Asp Ile Ser Met Phe Lys Ala Pro Ala Tyr Thr Leu His Ser
 60 65 70
 cgg cac tca gag aag cgg atg gtg tgc cac agc agc cct ggg cct tgc 412
 Arg His Ser Glu Lys Arg Met Val Cys His Ser Ser Pro Gly Pro Cys
 75 80 85
 tat ctc ttg gat ccc aaa ata act cgg ttt gga atg tcc agc tgc ccg 460
 Tyr Leu Leu Asp Pro Lys Ile Thr Arg Phe Gly Met Ser Ser Cys Pro
 90 95 100
 cag gtc ccc atg gag gag cgc atc tcc aac ctg cgc ctg aac ccc acc 508
 Gln Val Pro Met Glu Glu Arg Ile Ser Asn Leu Arg Leu Asn Pro Thr
 105 110 115

ctc gca tcc tgc cag tac tac ttt gag aag atc cac cca ccg ggg gaa 556
 Leu Ala Ser Cys Gln Tyr Tyr Phe Glu Lys Ile His Pro Pro Gly Glu
 120 125 130 135

cgc agg gct ccc cag tac acg ttt ggc tac cgg cgc cca tac aga gtg 604
 Arg Arg Ala Pro Gln Tyr Thr Phe Gly Tyr Arg Arg Pro Tyr Arg Val
 140 145 150

atg gac ctc aac ccg gct ccc aac cag tac cag atg cca ctc ttg ctg 652
 Met Asp Leu Asn Pro Ala Pro Asn Gln Tyr Gln Met Pro Leu Leu Leu
 155 160 165

ggg ccc aac acc cct gtc agc cga gct gct ccc tgc tac agt ctg gcc 700
 Gly Pro Asn Thr Pro Val Ser Arg Ala Ala Pro Cys Tyr Ser Leu Ala
 170 175 180

tcc agg gac aag aac tgg ttc tac aag gag gat gtg gca gga ggc cct 748
 Ser Arg Asp Lys Asn Trp Phe Tyr Lys Glu Asp Val Ala Gly Gly Pro
 185 190 195

gga cct acc acg tac gcc cga cct gag cca tcc atc tat cag aac cgc 796
 Gly Pro Thr Thr Tyr Ala Arg Pro Glu Pro Ser Ile Tyr Gln Asn Arg
 200 205 210 215

agc cct act tac agc atg gcc aag cgc ttc gcc tac cct ctg gac ctc 844
 Ser Pro Thr Tyr Ser Met Ala Lys Arg Phe Ala Tyr Pro Leu Asp Leu
 220 225 230

acg cca cgg cct ggc ccc ggc tcc cac gag gtc cag cag gtc act gtg 892
 Thr Pro Arg Pro Gly Pro Gly Ser His Glu Val Gln Gln Val Thr Val
 235 240 245

cac aag ccc cac atc cct gct ttc acc atg ggc atc aag cac tca ctc 940
 His Lys Pro His Ile Pro Ala Phe Thr Met Gly Ile Lys His Ser Leu
 250 255 260

cac ctg tgc cca ctg gtc atc gac att cgt gac tga ggccccctctt 986
 His Leu Cys Pro Leu Val Ile Asp Ile Arg Asp
 265 270

ggggcactca ctgccccctca tccccagaaa ttatttttct acaccaaatt gagcaatttg 1046

accaagatttt ctagtagcag agccggtacc tgctgagtgt ccggcacaca gaagacatta 1106

gagatacatt ttc 1119

<210> 90
 <211> 274
 <212> PRT
 <213> Homo sapiens

<400> 90
 Met Lys Leu Pro Lys Gly Thr Arg Ser Ser Val Tyr Phe Ala Gln His
 1 5 10 15
 Pro Glu Lys Glu Pro Leu Pro Ser Arg Gln Glu Val Lys Gln Thr Pro

Lys Glu Leu Leu Arg Ala Lys Leu Ile Glu Cys Gly Trp Lys Asp Gln
 30 35 40 45

ttg aag gca cac tgt aaa gag gta att aaa gaa aaa gga cta gaa cac 315
 Leu Lys Ala His Cys Lys Glu Val Ile Lys Glu Lys Gly Leu Glu His
 50 55 60

gtt act gtt gat gac ttg gtg gct gaa atc act cca aaa ggc aga gcc 363
 Val Thr Val Asp Asp Leu Val Ala Glu Ile Thr Pro Lys Gly Arg Ala
 65 70 75

ctg gta cct gac agt gta aag aag gag ctc cta caa aga ata aga aca 411
 Leu Val Pro Asp Ser Val Lys Lys Glu Leu Leu Gln Arg Ile Arg Thr
 80 85 90

ttc ctt gct cag cat gcc agc ctt taa gattgaatta gattgtgttg 458
 Phe Leu Ala Gln His Ala Ser Leu
 95 100

ttgtggtttt atttctgaaa gtaaaacttg ccataaatta gaaaacaatt tcccaaaaata 518

aaatcctttt ttgtatgatg gt 540

<210> 92
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 92
 Met Val Val Ser Lys Met Asn Lys Asp Ala Gln Met Arg Ala Ala Ile
 1 5 10 15
 Asn Gln Lys Leu Ile Glu Thr Gly Glu Arg Glu Arg Leu Lys Glu Leu
 20 25 30
 Leu Arg Ala Lys Leu Ile Glu Cys Gly Trp Lys Asp Gln Leu Lys Ala
 35 40 45
 His Cys Lys Glu Val Ile Lys Glu Lys Gly Leu Glu His Val Thr Val
 50 55 60
 Asp Asp Leu Val Ala Glu Ile Thr Pro Lys Gly Arg Ala Leu Val Pro
 65 70 75 80
 Asp Ser Val Lys Lys Glu Leu Leu Gln Arg Ile Arg Thr Phe Leu Ala
 85 90 95
 Gln His Ala Ser Leu
 100

<210> 93
 <211> 1059
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (33)..(869)

<400> 93
 gagttcctag taaagtggcg ggagccgcag ct atg gag ccg cag gag gag aga 53

	Met	Glu	Pro	Gln	Glu	Glu	Arg	
	1				5			
gaa acg cag gtt gct gcg tgg tta aaa aaa ata ttt gga gat cat cct 101								
Glu Thr Gln Val Ala Ala Trp Leu Lys Lys Ile Phe Gly Asp His Pro								
10 15 20								
att cca cag tat gag gtg aac cca cgg acc aca gag att tta cat cac 149								
Ile Pro Gln Tyr Glu Val Asn Pro Arg Thr Thr Glu Ile Leu His His								
25 30 35								
ctt tca gaa cgc aac agg gtc cgg gac agg gat gtc tac ctg gta ata 197								
Leu Ser Glu Arg Asn Arg Val Arg Asp Arg Asp Val Tyr Leu Val Ile								
40 45 50 55								
gag gac ttg aag cag aaa gca agt gaa tac gag tca gaa gcc aag tat 245								
Glu Asp Leu Lys Gln Lys Ala Ser Glu Tyr Glu Ser Glu Ala Lys Tyr								
60 65 70								
ctt caa gac ctt ctc atg gag agt gtg aat ttt tcc ccc gcc aat ctc 293								
Leu Gln Asp Leu Leu Met Glu Ser Val Asn Phe Ser Pro Ala Asn Leu								
75 80 85								
tct agc act ggt tcc agg tat ctg aat gct ttg gtt gac agt gcg gtg 341								
Ser Ser Thr Gly Ser Arg Tyr Leu Asn Ala Leu Val Asp Ser Ala Val								
90 95 100								
gcc ctt gaa aca aag gat acc tcg cta gct agt ttt atc cct gca gtg 389								
Ala Leu Glu Thr Lys Asp Thr Ser Leu Ala Ser Phe Ile Pro Ala Val								
105 110 115								
aat gat ttg acc tct gat ctc ttt cgt acc aaa tcc aaa agt gaa gaa 437								
Asn Asp Leu Thr Ser Asp Leu Phe Arg Thr Lys Ser Lys Ser Glu Glu								
120 125 130 135								
atc aag att gaa ctg gaa aaa ctt gaa aaa aat tta act gca act tta 485								
Ile Lys Ile Glu Leu Glu Lys Leu Glu Lys Asn Leu Thr Ala Thr Leu								
140 145 150								
gta tta gaa aaa tgt cta caa gag gat gtc aag aaa gca gag ttg cat 533								
Val Leu Glu Lys Cys Leu Gln Glu Asp Val Lys Lys Ala Glu Leu His								
155 160 165								
ctg tct aca gaa agg gcc aaa gtt gat aat cgt cgt cag aac atg gac 581								
Leu Ser Thr Glu Arg Ala Lys Val Asp Asn Arg Arg Gln Asn Met Asp								
170 175 180								
ttt cta aaa gca aag tca gag gaa ttc aga ttt gga atc aag gct gca 629								
Phe Leu Lys Ala Lys Ser Glu Glu Phe Arg Phe Gly Ile Lys Ala Ala								
185 190 195								
gag gag caa ctt tca gcc aga ggc atg gat gct tct ctg tct cat cag 677								
Glu Glu Gln Leu Ser Ala Arg Gly Met Asp Ala Ser Leu Ser His Gln								
200 205 210 215								
tcc tta gta gca cta tca gag aaa ctg gca aga tta aag caa cag act 725								
Ser Leu Val Ala Leu Ser Glu Lys Leu Ala Arg Leu Lys Gln Gln Thr								

220	225	230	
ata cct ttg aag aaa aaa ttg gag tcc tat tta gac tta atg ccg aat			773
Ile Pro Leu Lys Lys Lys Leu Glu Ser Tyr Leu Asp Leu Met Pro Asn			
235	240	245	
ccg tct ctt gct caa gtg aaa att gaa gaa gca aag cga gaa cta gat			821
Pro Ser Leu Ala Gln Val Lys Ile Glu Glu Ala Lys Arg Glu Leu Asp			
250	255	260	
agc att gaa gct gaa ctt aca aga aga gta gac atg atg gaa ctg tga			869
Ser Ile Glu Ala Glu Leu Thr Arg Arg Val Asp Met Met Glu Leu			
265	270	275	
caaaagccaa ataaacatcc ttttccctaa caaagtaa atg aataggac tttacagagt			929
tctttttcct cttggcattt cctaataaca aaactttctg tgttcttaga ttacagaata			989
tcataattga tagaatatgg tttcttactg tgtgttgc at tttgtgccc aaatacatag			1049
ttttcatatt			1059
<210> 94			
<211> 278			
<212> PRT			
<213> Homo sapiens			
<400> 94			
Met Glu Pro Gln Glu Glu Arg Glu Thr Gln Val Ala Ala Trp Leu Lys			
1 5 10 15			
Lys Ile Phe Gly Asp His Pro Ile Pro Gln Tyr Glu Val Asn Pro Arg			
20 25 30			
Thr Thr Glu Ile Leu His His Leu Ser Glu Arg Asn Arg Val Arg Asp			
35 40 45			
Arg Asp Val Tyr Leu Val Ile Glu Asp Leu Lys Gln Lys Ala Ser Glu			
50 55 60			
Tyr Glu Ser Glu Ala Lys Tyr Leu Gln Asp Leu Leu Met Glu Ser Val			
65 70 75 80			
Asn Phe Ser Pro Ala Asn Leu Ser Ser Thr Gly Ser Arg Tyr Leu Asn			
85 90 95			
Ala Leu Val Asp Ser Ala Val Ala Leu Glu Thr Lys Asp Thr Ser Leu			
100 105 110			
Ala Ser Phe Ile Pro Ala Val Asn Asp Leu Thr Ser Asp Leu Phe Arg			
115 120 125			
Thr Lys Ser Lys Ser Glu Glu Ile Lys Ile Glu Leu Glu Lys Leu Glu			
130 135 140			
Lys Asn Leu Thr Ala Thr Leu Val Leu Glu Lys Cys Leu Gln Glu Asp			
145 150 155 160			
Val Lys Lys Ala Glu Leu His Leu Ser Thr Glu Arg Ala Lys Val Asp			
165 170 175			
Asn Arg Arg Gln Asn Met Asp Phe Leu Lys Ala Lys Ser Glu Glu Phe			
180 185 190			
Arg Phe Gly Ile Lys Ala Ala Glu Glu Gln Leu Ser Ala Arg Gly Met			
195 200 205			
Asp Ala Ser Leu Ser His Gln Ser Leu Val Ala Leu Ser Glu Lys Leu			
210 215 220			

Ala Arg Leu Lys Gln Gln Thr Ile Pro Leu Lys Lys Lys Leu Glu Ser
 225 230 235 240
 Tyr Leu Asp Leu Met Pro Asn Pro Ser Leu Ala Gln Val Lys Ile Glu
 245 250 255
 Glu Ala Lys Arg Glu Leu Asp Ser Ile Glu Ala Glu Leu Thr Arg Arg
 260 265 270
 Val Asp Met Met Glu Leu
 275

<210> 95
 <211> 782
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (103)..(384)

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 accgccgccc tctgcccgcc ggcccgtctg tctaccccca gc atg agc ggc ctg 114
 Met Ser Gly Leu
 1
 cgc gtc tac agc acg tcg gtc acc ggc tcc cgc gaa atc aag tcc cag 162
 Arg Val Tyr Ser Thr Ser Val Thr Gly Ser Arg Glu Ile Lys Ser Gln
 5 10 15 20
 cag agc gag gtg acc cga atc ctg gat ggg aag cgc atc caa tac cag 210
 Gln Ser Glu Val Thr Arg Ile Leu Asp Gly Lys Arg Ile Gln Tyr Gln
 25 30 35
 cta gtg gac atc tcc cag gac aac gcc ctg agg gat gag atg cga gcc 258
 Leu Val Asp Ile Ser Gln Asp Asn Ala Leu Arg Asp Glu Met Arg Ala
 40 45 50
 ttg gca ggc aac ccc aag gcc acc cca ccc cag att gtc aac ggg gac 306
 Leu Ala Gly Asn Pro Lys Ala Thr Pro Pro Gln Ile Val Asn Gly Asp
 55 60 65
 cag tac tgt ggg gac tat gag ctg ttc gtg gag gct gtg gaa caa aac 354
 Gln Tyr Cys Gly Asp Tyr Glu Leu Phe Val Glu Ala Val Glu Gln Asn
 70 75 80
 acg ctg cag gag ttc ctg aag ctg gct tga gtcaagcctg tccagagttc 404
 Thr Leu Gln Glu Phe Leu Lys Leu Ala
 85 90
 ccctgctgga ctccatcacc acaactcccc cagccttcac ctggccatga aggacctttt 464
 gaccaactcc ctgtcattcc taacctaac ttagagtccc tcccccaatg caggccactt 524
 ctctccctc ctctctaaat gtagtcccct ctctccatc taaaggcaac attccttacc 584

cattagtctc agaaaattgtc ttaagcaaca gcccctaatg ctggctgccc ccagccaagc 644
attggggccc ccatcctgcc tggcactggc tgatgggcac ctctgttggt tccatcagcc 704
agagctctgc caaaggcccc gcagtccttc tcccaggagg accctagagg caattaaatg 764
atgtcctgtt ccattggc 782

<210> 96
<211> 93
<212> PRT
<213> Homo sapiens

<400> 96
Met Ser Gly Leu Arg Val Tyr Ser Thr Ser Val Thr Gly Ser Arg Glu
1 5 10 15
Ile Lys Ser Gln Gln Ser Glu Val Thr Arg Ile Leu Asp Gly Lys Arg
20 25 30
Ile Gln Tyr Gln Leu Val Asp Ile Ser Gln Asp Asn Ala Leu Arg Asp
35 40 45
Glu Met Arg Ala Leu Ala Gly Asn Pro Lys Ala Thr Pro Pro Gln Ile
50 55 60
Val Asn Gly Asp Gln Tyr Cys Gly Asp Tyr Glu Leu Phe Val Glu Ala
65 70 75 80
Val Glu Gln Asn Thr Leu Gln Glu Phe Leu Lys Leu Ala
85 90

<210> 97
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (22)..(195)

<400> 97
ctagagcgcc gcggccccga g atg aag ccg gcg gtg gac gag atg ttc ccc 51
Met Lys Pro Ala Val Asp Glu Met Phe Pro 10
1 5
gag ggc gcc ggg ccc tac gtg gac ctg gac gag gcg gga ggc agc acc 99
Glu Gly Ala Gly Pro Tyr Val Asp Leu Asp Glu Ala Gly Gly Ser Thr 25
15 20
ggg ctc ttg atg gac ttg gca gcc aat gaa aag gcc gtt cat gca gac 147
Gly Leu Leu Met Asp Leu Ala Ala Asn Glu Lys Ala Val His Ala Asp 40
30 35
ttt ttt aac gat ttt gaa gat ctt ttt gat gat gat gac atc cag tga 195
Phe Phe Asn Asp Phe Glu Asp Leu Phe Asp Asp Asp Asp Ile Gln 55
45 50
gatgccctct ggctgcaggc ggggccaagc ccttggtaca gagccgcagt gtgagcctgc 255

gcaggacagt ttccaggtggt ttttaagaac acgtggaaat cccttgaatt taggacctgg 315
 ttaaccagaa agataagact gttcttaacg acctagatga ttctgttcat ctctgaacgg 375
 gatcaggttt tgtcctcact ccaattaaaa gaaagcaatg tc 417

<210> 98
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 98
 Met Lys Pro Ala Val Asp Glu Met Phe Pro Glu Gly Ala Gly Pro Tyr
 1 5 10 15
 Val Asp Leu Asp Glu Ala Gly Gly Ser Thr Gly Leu Leu Met Asp Leu
 20 25 30
 Ala Ala Asn Glu Lys Ala Val His Ala Asp Phe Phe Asn Asp Phe Glu
 35 40 45
 Asp Leu Phe Asp Asp Asp Asp Ile Gln
 50 55

<210> 99
 <211> 697
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (65)..(412)

<400> 99
 aagacatttc ctgctcgaa ccttggttac taatttccac tgcttttaag gccctgcact 60
 gaaa atg caa gct cag gcg ccg gtg gtc gtt gtg acc caa cct gga gtc 109
 Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val
 1 5 10 15
 ggt ccc ggt ccg gcc ccc cag aac tcc aac tgg cag aca ggc atg tgt 157
 Gly Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys
 20 25 30
 gac tgt ttc agc gac tgc gga gtc tgt ctc tgt ggc aca ttt tgt ttc 205
 Asp Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe
 35 40 45
 ccg tgc ctt ggg tgt caa gtt gca gct gat atg aat gaa tgc tgt ctg 253
 Pro Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu
 50 55 60
 tgt gga aca agc gtc gca atg agg act ctc tac agg acc cga tat ggc 301
 Cys Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly
 65 70 75
 atc cct gga tct att tgt gat gac tat atg gca act ctt tgc tgt cct 349
 Ile Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro

05890688-092701

80 85 90 95
cat tgt act ctt tgc caa atc aag aga gat atc aac aga agg aga gcc 397
His Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala
100 105 110
atg cgt act ttc taa aaactgatgg tgaaaagctc ttaccgaagc aacaaaattc 452
Met Arg Thr Phe
115
agcagacacc tcttcagctt gagttcttca ccatcttttg caactgaaat atgatggata 512
tgcttaagta caactgatgg catgaaaaaa atcaaatttt tgatttatta taaatgaatg 572
ttgtccctga acttagctaa atggtgcaac ttagtttctc cttgctttca tattatcgaa 632
tttcctggct tataaacttt tttaaattaca ttgaaatat aaaccaaagc aaatatttta 692
ctgat 697

<210> 100
<211> 115
<212> PRT
<213> Homo sapiens

<400> 100
Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val Gly
1 5 10 15
Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys Asp
20 25 30
Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro
35 40 45
Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys
50 55 60
Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile
65 70 75 80
Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro His
85 90 95
Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met
100 105 110
Arg Thr Phe
115

<210> 101
<211> 1504
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (462)..(794)

<400> 101
tccgtctgtt ggggggcgaa cagccgcggt tctctgtcgt ggtgagcgca gccactcagg 60

[illegible]

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atgtgttttc aactcaggac ctatccaaat gaggaatttt taaatattct tttttttttc 1294
ctatttttag acatcaattc tatagattct gactttttct aacctcttat agacatgccca 1354
aatgctggca aaaagaagtg ctttttggat atggcagcac ttgtaaaaat aaagcagtaa 1414
gcaaaatcct tttaaacaca gaaatcctga gttcttctca ttggtggact caagcaattc 1474
tgtagcaaat aaatcctttg aaagagctcc 1504

<210> 102
<211> 110
<212> PRT
<213> Homo sapiens

<400> 102
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1 5 10 15
Ser Val Thr Gly Ser Gly Phe Ser Val Ser Asp Leu Ala Pro Pro Arg
20 25 30
Lys Ala Leu Phe Thr Tyr Pro Lys Gly Ala Gly Glu Met Leu Glu Asp
35 40 45
Gly Ser Glu Arg Phe Leu Cys Glu Ser Val Phe Ser Tyr Gln Val Ala
50 55 60
Ser Thr Leu Lys Gln Val Lys His Asp Gln Gln Val Ala Arg Met Glu
65 70 75 80
Lys Leu Ala Gly Leu Val Glu Glu Leu Glu Ala Asp Glu Trp Arg Phe
85 90 95
Lys Pro Ile Glu Gln Leu Leu Gly Phe Thr Pro Ser Ser Gly
100 105 110

<210> 103
<211> 1046
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (124)..(525)

<400> 103
tcgaggacat gatgacgtga ccctgagtgc ctggagccgt ctcttgattg ttcttcattt 60
ctgtttgtct gcttgcaatt ctggatcctg actgcccatg ggaggcatca gaccttcctt 120
ggg atg tgg tgt ggc tgt gat ggg aac ctg agt gtc cag acc tat tta 168
Met Trp Cys Gly Cys Asp Gly Asn Leu Ser Val Gln Thr Tyr Leu
1 5 10 15
ccg att gct cgt ggt ggg atc cct gcc ttc ctg ctg tgc ttg acc ccg 216
Pro Ile Ala Arg Gly Gly Ile Pro Ala Phe Leu Leu Cys Leu Thr Pro
20 25 30

ggt gtc cac gaa tgg tgt cct gac cct ctt ggg acg ctg aat gcc tgg 264
 Gly Val His Glu Trp Cys Pro Asp Pro Leu Gly Thr Leu Asn Ala Trp
 35 40 45

agc tgt ctc gtg cct gct cgt ggt gcg atc ctt gtc ttc ctc cag tgc 312
 Ser Cys Leu Val Pro Ala Arg Gly Ala Ile Leu Val Phe Leu Gln Cys
 50 55 60

tgg tcc cgg tcc gtc cat ggg cag agt cag gct gtt cat gag tgc tca 360
 Trp Ser Arg Ser Val His Gly Gln Ser Gln Ala Val His Glu Cys Ser
 65 70 75

cct ggt aga ggg aag acc ctg aac gtc cag acc gtt ccc ctg acc ggc 408
 Pro Gly Arg Gly Lys Thr Leu Asn Val Gln Thr Val Pro Leu Thr Gly
 80 85 90 95

cac gtg tgg act ctt ggt ggc tct gct gtc tca gcc cag cct ttc cgt 456
 His Val Trp Thr Leu Gly Gly Ser Ala Val Ser Ala Gln Pro Phe Arg
 100 105 110

ggc ctg aca ctg att gtg tgt ctg agt ttt ctg aat gtc cct cac tgt 504
 Gly Leu Thr Leu Ile Val Cys Leu Ser Phe Leu Asn Val Pro His Cys
 115 120 125

cac tgg cct gac tac cgc tag acccccggtg tccacgatcg ctgactgcag 555
 His Trp Pro Asp Tyr Arg
 130

atgaagcttg cccgcgcccc gtggctgagt gtctggagct gtctgctgac tgctggtggc 615
 cggatccatg tctttctcct ggacttgatc ttgcctgttc atgggatgat gcagtctgtc 675
 cacgagagga agtctctgcg tgacgagtgc ctgattgtct ggagctgtct gcagagtgcc 735
 catgactggc tctgtcttca tcatgggacc tgggggtgtct ggagccatct cttgactgct 795
 cccacgcaga tccatgatgg tttctggaag ccgaccaga gtgcctctca gagtcttctg 855
 agtgtccctc actgtccctg tctctggctaa ctctggatcc cctacgcttt cttgtcctgg 915
 actcctgcaa tggtagctgg cttgtatttt catgtcttga cctgttcact tgagatgatg 975
 atttgccatc agatgacctt gatctttcat atattttgtt ttctttctaat agactatcag 1035
 tgggtgcata g 1046

<210> 104
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Trp Cys Gly Cys Asp Gly Asn Leu Ser Val Gln Thr Tyr Leu Pro
 1 5 10 15
 Ile Ala Arg Gly Gly Ile Pro Ala Phe Leu Leu Cys Leu Thr Pro Gly

<210> 106
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> residue
 <222> (9)
 <223> Xaa = selenocysteine

<400> 106
 Met Cys Tyr Asp Leu Gly Thr Asn Xaa Ala Thr Ser Val Ala Leu Arg
 1 5 10 15
 Ala Val Arg Thr Leu Gln Ala Gly Gln Val Pro Gly Arg Pro Gly Leu
 20 25 30
 Ala Tyr Ala Pro Leu Cys Pro Leu Ala Phe Lys Gly Phe Phe Pro Asn
 35 40 45
 Leu Arg Pro Ser Ala Thr Cys Arg Phe Arg Arg Glu Pro Ala Ala Ser
 50 55 60
 Phe Glu Pro Lys
 65

<210> 107
 <211> 1684
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(1011)

<400> 107
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 Met Ala Ser Gly Leu Val Arg Leu Leu Gln Gln Gly His
 1 5 10

 cgc tgc ctc ctg gct cca gtc gcc ccc aag ctg gtc cct ccg gtt cgg 99
 Arg Cys Leu Leu Ala Pro Val Ala Pro Lys Leu Val Pro Pro Val Arg
 15 20 25

 gga gtg aag aag gga ttc cgc gcc gcc ttc cgc ttc cag aag gag tta 147
 Gly Val Lys Lys Gly Phe Arg Ala Ala Phe Arg Phe Gln Lys Glu Leu
 30 35 40 45

 gag cgg cag cgc ctt ctg cgg tgc ccg ccg ccg ccc gtg cgc cgt tca 195
 Glu Arg Gln Arg Leu Leu Arg Cys Pro Pro Pro Pro Val Arg Arg Ser
 50 55 60

 gag aag ccg aac tgg gat tac cat gca gaa ata caa gct ttt gga cat 243
 Glu Lys Pro Asn Trp Asp Tyr His Ala Glu Ile Gln Ala Phe Gly His
 65 70 75

 cgg tta cag gaa aac ttt tcc tta gat ctt ctc aaa act gca ttt gtt 291
 Arg Leu Gln Glu Asn Phe Ser Leu Asp Leu Leu Lys Thr Ala Phe Val

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80					85					90									
aat	agc	tgc	tat	att	aaa	agt	gag	gag	gcc	aaa	cgc	caa	caa	ctt	ggg	339			
Asn	Ser	Cys	Tyr	Ile	Lys	Ser	Glu	Glu	Ala	Lys	Arg	Gln	Gln	Leu	Gly				
95					100					105									
ata	gag	aaa	gaa	gct	gtt	ctt	ctg	aat	ctt	aaa	agt	aat	caa	gaa	cta	387			
Ile	Glu	Lys	Glu	Ala	Val	Leu	Leu	Asn	Leu	Lys	Ser	Asn	Gln	Glu	Leu				
110					115					120					125				
tcc	gaa	caa	ggg	aca	tct	ttt	tca	cag	act	tgc	ctt	aca	cag	ttt	ctt	435			
Ser	Glu	Gln	Gly	Thr	Ser	Phe	Ser	Gln	Thr	Cys	Leu	Thr	Gln	Phe	Leu				
130					135					140									
gaa	gac	gag	tac	cca	gac	atg	ccc	act	gaa	ggc	ata	aaa	aat	ctt	gtt	483			
Glu	Asp	Glu	Tyr	Pro	Asp	Met	Pro	Thr	Glu	Gly	Ile	Lys	Asn	Leu	Val				
145					150					155									
gac	ttt	ctc	act	ggg	gag	gaa	gtc	gtg	tgt	cac	gtg	gct	aga	aac	ttg	531			
Asp	Phe	Leu	Thr	Gly	Glu	Glu	Val	Val	Cys	His	Val	Ala	Arg	Asn	Leu				
160					165					170									
gct	gtg	gag	cag	tta	aca	ctg	agt	gaa	gaa	ttc	cca	gtg	ccc	cca	gct	579			
Ala	Val	Glu	Gln	Leu	Thr	Leu	Ser	Glu	Glu	Phe	Pro	Val	Pro	Pro	Ala				
175					180					185									
gtg	tta	cag	cag	act	ttc	ttt	gca	gtt	att	gga	gcc	ctg	tta	cag	agc	627			
Val	Leu	Gln	Gln	Thr	Phe	Phe	Ala	Val	Ile	Gly	Ala	Leu	Leu	Gln	Ser				
190					195					200					205				
agt	gga	cct	gag	agg	act	gca	ctt	ttc	atc	agg	gac	ttc	tta	att	act	675			
Ser	Gly	Pro	Glu	Arg	Thr	Ala	Leu	Phe	Ile	Arg	Asp	Phe	Leu	Ile	Thr				
210					215					220									
caa	atg	act	gga	aaa	gag	ctc	ttt	gag	atg	tgg	aag	ata	ata	aat	ccc	723			
Gln	Met	Thr	Gly	Lys	Glu	Leu	Phe	Glu	Met	Trp	Lys	Ile	Ile	Asn	Pro				
225					230					235									
atg	ggg	cta	ttg	gta	gaa	gaa	ctg	aag	aaa	agg	aat	gtt	tca	gct	cct	771			
Met	Gly	Leu	Leu	Val	Glu	Glu	Leu	Lys	Lys	Arg	Asn	Val	Ser	Ala	Pro				
240					245					250									
gaa	tca	aga	ctt	act	agg	cag	tct	ggg	ggc	acc	aca	gct	ttg	cct	ttg	819			
Glu	Ser	Arg	Leu	Thr	Arg	Gln	Ser	Gly	Gly	Thr	Thr	Ala	Leu	Pro	Leu				
255					260					265									
tat	ttt	gtt	ggc	tta	tac	tgt	gat	aaa	aag	ttg	att	gca	gaa	gga	cct	867			
Tyr	Phe	Val	Gly	Leu	Tyr	Cys	Asp	Lys	Lys	Leu	Ile	Ala	Glu	Gly	Pro				
270					275					280					285				
ggg	gaa	aca	gta	ttg	gtt	gca	gaa	gaa	gag	gct	gct	cga	gtg	gcc	ctt	915			
Gly	Glu	Thr	Val	Leu	Val	Ala	Glu	Glu	Glu	Ala	Ala	Arg	Val	Ala	Leu				
290					295					300									
aga	aaa	ctt	tat	gga	ttc	aca	gaa	aat	aga	cgg	ccg	tgg	aac	tat	tcc	963			
Arg	Lys	Leu	Tyr	Gly	Phe	Thr	Glu	Asn	Arg	Arg	Pro	Trp	Asn	Tyr	Ser				
305					310					315									

aag ccc aaa gaa acc ttg aga gca gaa aag agc atc act gcc agc tag 1011
 Lys Pro Lys Glu Thr Leu Arg Ala Glu Lys Ser Ile Thr Ala Ser
 320 325 330

ccgccatgga tgcagcagcc tgaaacttga gagcgaaagt gagataaatg tcaaaggtgt 1071
 ttcaagccag acatttttcac aattgtgaag aaatagatgt tttgtttctg ttttttactg 1131
 tgttcccaaa attaaataaa tgtaaccaa gtcacagtgt ttttggtttt gtttttctga 1191
 aatcttggtt tgatcaaatac tttttttttt tctcttgaga tggagtctta ctctgtcgcc 1251
 caggctggac tgcagtgggtg cgatctcggc tcaactgcaac ctccacctca caggttcaag 1311
 cgattctcgt ggctcagcct ccctagtagc tgggattaca ggcacacacc accatacctg 1371
 gctaattttt gtatttttgg tagacatggg gtttcaccaa gttggctagg ctagtcttga 1431
 actcctgacc tcaggtgatc caccgcctt ggcctcccaa agtgctggga ttacaggtgt 1491
 gagccactat acccgaccag atcaaatac tttttgacat ttttgcaaaa aaattttcct 1551
 aatgttcttg atttaattgt atagaatttg tataattagg tgtattttat ttgcgtctag 1611
 ctttgaggta tcataattta tgtatcttat gtgaattttt tgctgtaata ccaataaagt 1671
 tttttttctc cac 1684

<210> 108
 <211> 332
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Ala Ser Gly Leu Val Arg Leu Leu Gln Gln Gly His Arg Cys Leu
 1 5 10 15
 Leu Ala Pro Val Ala Pro Lys Leu Val Pro Pro Val Arg Gly Val Lys
 20 25 30
 Lys Gly Phe Arg Ala Ala Phe Arg Phe Gln Lys Glu Leu Glu Arg Gln
 35 40 45
 Arg Leu Leu Arg Cys Pro Pro Pro Pro Val Arg Arg Ser Glu Lys Pro
 50 55 60
 Asn Trp Asp Tyr His Ala Glu Ile Gln Ala Phe Gly His Arg Leu Gln
 65 70 75 80
 Glu Asn Phe Ser Leu Asp Leu Leu Lys Thr Ala Phe Val Asn Ser Cys
 85 90 95
 Tyr Ile Lys Ser Glu Glu Ala Lys Arg Gln Gln Leu Gly Ile Glu Lys
 100 105 110
 Glu Ala Val Leu Leu Asn Leu Lys Ser Asn Gln Glu Leu Ser Glu Gln
 115 120 125
 Gly Thr Ser Phe Ser Gln Thr Cys Leu Thr Gln Phe Leu Glu Asp Glu
 130 135 140
 Tyr Pro Asp Met Pro Thr Glu Gly Ile Lys Asn Leu Val Asp Phe Leu
 145 150 155 160
 Thr Gly Glu Glu Val Val Cys His Val Ala Arg Asn Leu Ala Val Glu

				165				170					175			
Gln	Leu	Thr	Leu	Ser	Glu	Glu	Phe	Pro	Val	Pro	Pro	Ala	Val	Leu	Gln	
			180					185					190			
Gln	Thr	Phe	Phe	Ala	Val	Ile	Gly	Ala	Leu	Leu	Gln	Ser	Ser	Gly	Pro	
		195					200					205				
Glu	Arg	Thr	Ala	Leu	Phe	Ile	Arg	Asp	Phe	Leu	Ile	Thr	Gln	Met	Thr	
	210					215					220					
Gly	Lys	Glu	Leu	Phe	Glu	Met	Trp	Lys	Ile	Ile	Asn	Pro	Met	Gly	Leu	
225					230					235					240	
Leu	Val	Glu	Glu	Leu	Lys	Lys	Arg	Asn	Val	Ser	Ala	Pro	Glu	Ser	Arg	
				245					250					255		
Leu	Thr	Arg	Gln	Ser	Gly	Gly	Thr	Thr	Ala	Leu	Pro	Leu	Tyr	Phe	Val	
			260					265					270			
Gly	Leu	Tyr	Cys	Asp	Lys	Lys	Leu	Ile	Ala	Glu	Gly	Pro	Gly	Glu	Thr	
		275					280					285				
Val	Leu	Val	Ala	Glu	Glu	Glu	Ala	Ala	Arg	Val	Ala	Leu	Arg	Lys	Leu	
	290					295					300					
Tyr	Gly	Phe	Thr	Glu	Asn	Arg	Arg	Pro	Trp	Asn	Tyr	Ser	Lys	Pro	Lys	
305					310					315					320	
Glu	Thr	Leu	Arg	Ala	Glu	Lys	Ser	Ile	Thr	Ala	Ser					
				325					330							

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<210> 109
<211> 727
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (81)..(560)
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gccccggacc aggtgcctcc atg gca ggc tct gaa gag ctg ggg ctc cgg gaa 113
Met Ala Gly Ser Glu Glu Leu Gly Leu Arg Glu
1 5 10

gac acg ctg agg gtc cta gct gcc ttc ctt agg cgt ggt gag gct gcc 161
Asp Thr Leu Arg Val Leu Ala Ala Phe Leu Arg Arg Gly Glu Ala Ala
15 20 25

ggg tct cct gtt cca act cca cct aga agc cct gcc caa gaa gag cca 209
Gly Ser Pro Val Pro Thr Pro Pro Arg Ser Pro Ala Gln Glu Glu Pro
30 35 40

aca gac ttc ctg agc cgc ctt cga aga tgt ctt ccc tgc tcc ctg ggg 257
Thr Asp Phe Leu Ser Arg Leu Arg Arg Cys Leu Pro Cys Ser Leu Gly
45 50 55

cga gga gca gcc ccc tct gag tcc cct cgg cct tgc tct ctg ccc atc 305
Arg Gly Ala Ala Pro Ser Glu Ser Pro Arg Pro Cys Ser Leu Pro Ile
60 65 70 75

cgc ccc tgc tat ggt tta gag cct ggc cca gct act cca gac ttc tat 353
Arg Pro Cys Tyr Gly Leu Glu Pro Gly Pro Ala Thr Pro Asp Phe Tyr

80	85	90	
gct ttg gtg gcc cag cgg ctg gaa cag ctg gtc caa gag cag ctg aaa			401
Ala Leu Val Ala Gln Arg Leu Glu Gln Leu Val Gln Glu Gln Leu Lys			
95	100	105	
tct ccg ccc agc cca gaa tta cag ggt ccc cca tcg aca gag aag gaa			449
Ser Pro Pro Ser Pro Glu Leu Gln Gly Pro Pro Ser Thr Glu Lys Glu			
110	115	120	
gcc ata ctg cgg agg ctg gtg gcc ctg ctg gag gag gag gca gaa gtc			497
Ala Ile Leu Arg Arg Leu Val Ala Leu Leu Glu Glu Glu Ala Glu Val			
125	130	135	
att aac cag aag gag ggc atc ctg gct gtt tca ccc gtg gac ttg aac			545
Ile Asn Gln Lys Glu Gly Ile Leu Ala Val Ser Pro Val Asp Leu Asn			
140	145	150	155
ttg cca ttg gac tga gctctttctc agaagctgct acaagatgac acctcatgtc			600
Leu Pro Leu Asp			
cctgccctct tcgtgtgctt ttccaagtct tectattcca ctcagggctg tgggggtggtg			660
gttgccctac ctgtttttgc caaaaataaa ttgttttaaaa cttttcttat taaaaacgtt			720
acaaagt			727
<210> 110			
<211> 159			
<212> PRT			
<213> Homo sapiens			
<400> 110			
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1 5 10 15			
Leu Ala Ala Phe Leu Arg Arg Gly Glu Ala Ala Gly Ser Pro Val Pro			
20 25 30			
Thr Pro Pro Arg Ser Pro Ala Gln Glu Glu Pro Thr Asp Phe Leu Ser			
35 40 45			
Arg Leu Arg Arg Cys Leu Pro Cys Ser Leu Gly Arg Gly Ala Ala Pro			
50 55 60			
Ser Glu Ser Pro Arg Pro Cys Ser Leu Pro Ile Arg Pro Cys Tyr Gly			
65 70 75 80			
Leu Glu Pro Gly Pro Ala Thr Pro Asp Phe Tyr Ala Leu Val Ala Gln			
85 90 95			
Arg Leu Glu Gln Leu Val Gln Glu Gln Leu Lys Ser Pro Pro Ser Pro			
100 105 110			
Glu Leu Gln Gly Pro Pro Ser Thr Glu Lys Glu Ala Ile Leu Arg Arg			
115 120 125			
Leu Val Ala Leu Leu Glu Glu Ala Glu Val Ile Asn Gln Lys Glu			
130 135 140			
Gly Ile Leu Ala Val Ser Pro Val Asp Leu Asn Leu Pro Leu Asp			
145 150 155			

<210> 111
 <211> 1354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (133)..(870)

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 acccctcccc ctccccgcgg taccttgacac ttttctccct ccttgcccc tctcgagtcc 60

accctccggg ccttctgccc ctgatcgctt gggtttccct gcagtcgcct gctgctgtcg 120

tcgggaggaa ag atg aat ggg agg gct gat ttt cga gag ccg aat gca gag 171
 Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala Glu
 1 5 10

gtt cca aga cca att ccc cac ata ggg cct gat tac att cca aca gag 219
 Val Pro Arg Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr Glu
 15 20 25

gaa gaa agg aga gtc ttc gca gaa tgc aat gat gaa agc ttc tgg ttc 267
 Glu Glu Arg Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp Phe
 30 35 40 45

aga tct gtg cct ttg gct gca aca agt atg ttg att act caa gga tta 315
 Arg Ser Val Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly Leu
 50 55 60

att agt aaa gga ata ctt tca agt cat ccc aaa tat ggt tcc atc cct 363
 Ile Ser Lys Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile Pro
 65 70 75

aaa ctt ata ctt gct tgt atc atg gga tac ttt gct gga aaa ctt tct 411
 Lys Leu Ile Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu Ser
 80 85 90

tat gtg aaa act tgc caa gag aaa ttc aag aaa ctt gaa aat tcc ccc 459
 Tyr Val Lys Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser Pro
 95 100 105

ctt gga gaa gct tta cga tca gga caa gca cga cga tct tca cca cct 507
 Leu Gly Glu Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro Pro
 110 115 120 125

ggg cac tat tat caa aag tca aaa tat gac tca agt gtg agt ggt caa 555
 Gly His Tyr Tyr Gln Lys Ser Lys Tyr Asp Ser Ser Val Ser Gly Gln
 130 135 140

tca tct ttt gtg aca tcc cca gca gca gac aac ata gaa atg ctt cct 603
 Ser Ser Phe Val Thr Ser Pro Ala Ala Asp Asn Ile Glu Met Leu Pro
 145 150 155

cat tat gag cca att cca ttc agt tct tct atg aat gaa tct gct ccc 651
 His Tyr Glu Pro Ile Pro Phe Ser Ser Ser Met Asn Glu Ser Ala Pro
 160 165 170

act ggt att act gat cat att gtc caa gga cct gat ccc aac ctt gaa 699
Thr Gly Ile Thr Asp His Ile Val Gln Gly Pro Asp Pro Asn Leu Glu
175 180 185

gaa agt cct aaa aga aaa aat att aca tat gag gaa tta agg aat aag 747
Glu Ser Pro Lys Arg Lys Asn Ile Thr Tyr Glu Glu Leu Arg Asn Lys
190 195 200 205

aac aga gag tca tat gaa gta tct tta aca caa aag act gac ccc tca 795
Asn Arg Glu Ser Tyr Glu Val Ser Leu Thr Gln Lys Thr Asp Pro Ser
210 215 220

gtc agg cct atg cat gaa aga gtg cca aaa aaa gaa gtc aaa gta aac 843
Val Arg Pro Met His Glu Arg Val Pro Lys Lys Glu Val Lys Val Asn
225 230 235

aag tat gga gat act tgg gat gag tga aaaattacat cattggacat 890
Lys Tyr Gly Asp Thr Trp Asp Glu
240 245

gaaggagttt caacatccag cttcatctag gtgggtcatga ttacctgcat gctttgagct 950
cagcagcagt cttcataaac acatttaaaa caagatcctg gggttttgtg gtttgacttc 1010
tatggtgttt taaaaaaaca cagattttta gtgttaatat tgtgtaaatg tactcacctt 1070
agggattcat ttgaatgatg gtattataacc atgattgtat acagtttgtg aaattgttgc 1130
aagggcaaag ataactctta aaaaaccgtc gagattacaa tgctctagaa tcagcatata 1190
agaaaataaa tgatatctgc atgttgaatt ggggtggatg gggggagcaa gcataatttt 1250
taagtgtgaa gctttgcatc aagaaattat taaaaagctt tttttctcca gtattttctg 1310
tattatctta atgtttatgg caaataaaat gtaaaggaac atgc 1354

<210> 112
<211> 245
<212> PRT
<213> Homo sapiens

<400> 112
Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala Glu Val Pro Arg
1 5 10 15
Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr Glu Glu Glu Arg
20 25 30
Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp Phe Arg Ser Val
35 40 45
Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly Leu Ile Ser Lys
50 55 60
Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile Pro Lys Leu Ile
65 70 75 80
Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu Ser Tyr Val Lys
85 90 95
Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser Pro Leu Gly Glu

	100		105		110									
Ala	Leu	Arg	Ser	Gly	Gln	Ala	Arg	Ser	Ser	Pro	Pro	Gly	His	Tyr
	115		120		125									
Tyr	Gln	Lys	Ser	Lys	Tyr	Asp	Ser	Ser	Val	Ser	Gly	Gln	Ser	Phe
	130		135		140									
Val	Thr	Ser	Pro	Ala	Ala	Asp	Asn	Ile	Glu	Met	Leu	Pro	His	Tyr
	145		150		155									
Pro	Ile	Pro	Phe	Ser	Ser	Ser	Met	Asn	Glu	Ser	Ala	Pro	Thr	Gly
	165		170		175									
Thr	Asp	His	Ile	Val	Gln	Gly	Pro	Asp	Pro	Asn	Leu	Glu	Glu	Ser
	180		185		190									
Lys	Arg	Lys	Asn	Ile	Thr	Tyr	Glu	Glu	Leu	Arg	Asn	Lys	Asn	Arg
	195		200		205									
Ser	Tyr	Glu	Val	Ser	Leu	Thr	Gln	Lys	Thr	Asp	Pro	Ser	Val	Arg
	210		215		220									
Met	His	Glu	Arg	Val	Pro	Lys	Lys	Glu	Val	Lys	Val	Asn	Lys	Tyr
	225		230		235									
Asp	Thr	Trp	Asp	Glu										
	245													

<210> 113
 <211> 653
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (170)..(502)

<400> 113
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 aattggctac cggaaaaaac caggctgggc tgggcgccgc catgacaacc gataccggaa 120
 aaggcgggtc gttccccccg gacagcccta cgccggcaaa ggtctcgag atg cag gcg 178
 Met Gln Ala
 1

gcc cta gag gtc acc gct cgc tac tgt ggc cgg gag ctg gag cag tat 226
 Ala Leu Glu Val Thr Ala Arg Tyr Cys Gly Arg Glu Leu Glu Gln Tyr
 5 10 15

ggc cag tgt gtg gcg gcc aag ccg gaa tcc tgg cag cgg gac tgt cac 274
 Gly Gln Cys Val Ala Ala Lys Pro Glu Ser Trp Gln Arg Asp Cys His
 20 25 30 35

tac ctt aag atg agc att gcc cag tgc aca tcc tcc cac cca atc atc 322
 Tyr Leu Lys Met Ser Ile Ala Gln Cys Thr Ser Ser His Pro Ile Ile
 40 45 50

cgc cag atc cgc cag gcc tgt gct cag cct ttt gag gcc ttc gag gag 370
 Arg Gln Ile Arg Gln Ala Cys Ala Gln Pro Phe Glu Ala Phe Glu Glu
 55 60 65

tgt ctt cga cag aac gag gca gct gtg ggc aac tgt gca gag cat atg 418
 Cys Leu Arg Gln Asn Glu Ala Ala Val Gly Asn Cys Ala Glu His Met

70 75 80

cgc cgc ttc ctg cag tgc gct gag cag gtg cag ccg cca cgc tca cct 466
 Arg Arg Phe Leu Gln Cys Ala Glu Gln Val Gln Pro Pro Arg Ser Pro
 85 90 95

gca act gtg gag gca cag cca ctt cct gcc tcc tga ggactcctct 512
 Ala Thr Val Glu Ala Gln Pro Leu Pro Ala Ser
 100 105 110

gacggcagga aaactggaca tgaatgactg cccccccgcc cctccctgc agagtggcca 572

gatggagtcc tgagccctgg acatggggccc ggctttcctg gatatcagga cttccaataa 632

ataaagactc tgtatactgg g 653

<210> 114
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 114

Met	Gln	Ala	Ala	Leu	Glu	Val	Thr	Ala	Arg	Tyr	Cys	Gly	Arg	Glu	Leu
1				5					10					15	
Glu	Gln	Tyr	Gly	Gln	Cys	Val	Ala	Ala	Lys	Pro	Glu	Ser	Trp	Gln	Arg
			20					25					30		
Asp	Cys	His	Tyr	Leu	Lys	Met	Ser	Ile	Ala	Gln	Cys	Thr	Ser	Ser	His
		35				40						45			
Pro	Ile	Ile	Arg	Gln	Ile	Arg	Gln	Ala	Cys	Ala	Gln	Pro	Phe	Glu	Ala
	50				55						60				
Phe	Glu	Glu	Cys	Leu	Arg	Gln	Asn	Glu	Ala	Ala	Val	Gly	Asn	Cys	Ala
65				70					75						80
Glu	His	Met	Arg	Arg	Phe	Leu	Gln	Cys	Ala	Glu	Gln	Val	Gln	Pro	Pro
			85					90						95	
Arg	Ser	Pro	Ala	Thr	Val	Glu	Ala	Gln	Pro	Leu	Pro	Ala	Ser		
			100				105						110		

<210> 115
 <211> 643
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (40)..(411)

<400> 115

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 Met Gly Ala Pro Gly
 1 5

gga aag atc aac cgg ccc cga acg gag ctg aag aag aag ctg ttc aaa 102
 Gly Lys Ile Asn Arg Pro Arg Thr Glu Leu Lys Lys Lys Leu Phe Lys
 10 15 20

cgc cgg cgg gtg ttg aat cgg gag cgg cgt ctg agg cac cgg gtg gtc 150
 Arg Arg Arg Val Leu Asn Arg Glu Arg Arg Leu Arg His Arg Val Val
 25 30 35

 ggg gct gtg ata gac caa ggg ctg atc acg cgg cac cac ctc aag aag 198
 Gly Ala Val Ile Asp Gln Gly Leu Ile Thr Arg His His Leu Lys Lys
 40 45 50

 cgg gcg tcc agt gca cgt gcc aac att aca ctg tca ggg aag aag cgc 246
 Arg Ala Ser Ser Ala Arg Ala Asn Ile Thr Leu Ser Gly Lys Lys Arg
 55 60 65

 aga aaa ctc ctc cag cag atc cgg ctt gcc cag aaa gag aag aca gcc 294
 Arg Lys Leu Leu Gln Gln Ile Arg Leu Ala Gln Lys Glu Lys Thr Ala
 70 75 80 85

 atg gaa gtg gaa gcc cct tca aag cca gcc agg act agt gaa cca cag 342
 Met Glu Val Glu Ala Pro Ser Lys Pro Ala Arg Thr Ser Glu Pro Gln
 90 95 100

 ctc aaa agg caa aag aag aca aaa gcc ccc cag gat gta gaa atg aag 390
 Leu Lys Arg Gln Lys Lys Thr Lys Ala Pro Gln Asp Val Glu Met Lys
 105 110 115

 gac ctt gaa gat gag agc taa acctcttcca ctagaagatt ctcaactgga 441
 Asp Leu Glu Asp Glu Ser
 120

 gccagccttc agactcagtg gttgtttcag aggactttga caaaagcaag gcccttttc 501
 actctccaga tttcctccta cctaattggcc tactgacctc ccctagaggg atgtcttttg 561
 gaggggaagaa ggtacagaag aaagattgga gaagggtctc tctagcagtc aactccattt 621
 gtaataaagc cctagcactc tg 643

<210> 116
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Gly Ala Pro Gly Gly Lys Ile Asn Arg Pro Arg Thr Glu Leu Lys
 1 5 10 15
 Lys Lys Leu Phe Lys Arg Arg Arg Val Leu Asn Arg Glu Arg Arg Leu
 20 25 30
 Arg His Arg Val Val Gly Ala Val Ile Asp Gln Gly Leu Ile Thr Arg
 35 40 45
 His His Leu Lys Lys Arg Ala Ser Ser Ala Arg Ala Asn Ile Thr Leu
 50 55 60
 Ser Gly Lys Lys Arg Arg Lys Leu Leu Gln Gln Ile Arg Leu Ala Gln
 65 70 75 80
 Lys Glu Lys Thr Ala Met Glu Val Glu Ala Pro Ser Lys Pro Ala Arg
 85 90 95
 Thr Ser Glu Pro Gln Leu Lys Arg Gln Lys Lys Thr Lys Ala Pro Gln
 100 105 110

Asp Val Glu Met Lys Asp Leu Glu Asp Glu Ser
115 120

<210> 117
<211> 1293
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (306)..(1019)

<400> 117
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cctcccgggtg agaacgaacc gcagtgtcca ccggcgagga gccagccctg tcccgggtcag 120
agaaagacga cgaggatacc tgggagcggg ccggcgccgg gctgggccgc gccggtgcgg 180
gctggcgact ctgctcctcc gcttgctgct gtctctggga actgggtgcc agcgctgagg 240
ggcttccagc ggacagggac ccccttcccc ggctcccctg cccaccctgc cggggagggc 300
ggaag atg ccg gtg aag aag aag aga aaa tcc cct ggg gtg gca gca gca 350
Met Pro Val Lys Lys Lys Arg Lys Ser Pro Gly Val Ala Ala Ala
1 5 10 15
gta gcg gaa gac gga ggc ctc aaa aag tgt aaa atc tcc agc tat tgc 398
Val Ala Glu Asp Gly Gly Leu Lys Lys Cys Lys Ile Ser Ser Tyr Cys
20 25 30
aga tcc caa ccc cct gct aga cta ata agt gga gag gaa cat ttt tca 446
Arg Ser Gln Pro Pro Ala Arg Leu Ile Ser Gly Glu Glu His Phe Ser
35 40 45
agc aag aag tgc ctg gct tgg ttt tat gaa tat gca ggt cct gat gaa 494
Ser Lys Lys Cys Leu Ala Trp Phe Tyr Glu Tyr Ala Gly Pro Asp Glu
50 55 60
gtt gta ggg cca gaa gga atg gaa aaa ttt tgt gaa gac att ggt gtt 542
Val Val Gly Pro Glu Gly Met Glu Lys Phe Cys Glu Asp Ile Gly Val
65 70 75
gaa cct gaa aat att att atg tta gtt tta gcg tgg aaa ttg gag gct 590
Glu Pro Glu Asn Ile Ile Met Leu Val Leu Ala Trp Lys Leu Glu Ala
80 85 90 95
gaa agc atg gga ttt ttt acc aag gaa gaa tgg tta aag gga atg act 638
Glu Ser Met Gly Phe Phe Thr Lys Glu Glu Trp Leu Lys Gly Met Thr
100 105 110
tca tta cag tgt gac tgc aca gaa aag tta caa aac aaa ttt gac ttt 686
Ser Leu Gln Cys Asp Cys Thr Glu Lys Leu Gln Asn Lys Phe Asp Phe
115 120 125
ttg cgc tca cag ttg aat gat att tcg tca ttt aag aat atc tac aga 734

Leu Arg Ser Gln Leu Asn Asp Ile Ser Ser Phe Lys Asn Ile Tyr Arg
 130 135 140

tat gcc ttt gat ttt gca agg gat aaa gat cag aga agc ctt gat att 782
 Tyr Ala Phe Asp Phe Ala Arg Asp Lys Asp Gln Arg Ser Leu Asp Ile
 145 150 155

gat act gct aaa tct atg tta gct ctt ctg ctt ggg agg aca tgg cca 830
 Asp Thr Ala Lys Ser Met Leu Ala Leu Leu Leu Gly Arg Thr Trp Pro
 160 165 170 175

ctg ttt tca gta ttt tac cag tac ctg gag caa tca aag tat cgt gtt 878
 Leu Phe Ser Val Phe Tyr Gln Tyr Leu Glu Gln Ser Lys Tyr Arg Val
 180 185 190

atg aac aaa gat caa tgg tac aat gta tta gaa ttc agc aga aca gtc 926
 Met Asn Lys Asp Gln Trp Tyr Asn Val Leu Glu Phe Ser Arg Thr Val
 195 200 205

cat gct gat ctt agt aac tat gat gaa gat ggt gct tgg cct gtt ctt 974
 His Ala Asp Leu Ser Asn Tyr Asp Glu Asp Gly Ala Trp Pro Val Leu
 210 215 220

ctt gat gaa ttt gtt gag tgg caa aaa gtc cgt cag aca tca tag 1019
 Leu Asp Glu Phe Val Glu Trp Gln Lys Val Arg Gln Thr Ser
 225 230 235

caagaactat gtgaagaaaa tgcaaaccctt tcaattccca cgtgtataca agctaattgtg 1079

atgaggggga aaaaaatcca acgggtgcat tttcattcat atgaaagact tctcatagta 1139

cttttttttc ctttttttaa aggaggtttt tcttggtaca tgtgatgggc attgagccac 1199

acctcttctt agactgaata ttgaagtttt tgttttgagt tatgtttata acattttattt 1259

cagaacaata aagattcaga tttgtgacaa aggc 1293

<210> 118
 <211> 237
 <212> PRT
 <213> Homo sapiens

<400> 118
 Met Pro Val Lys Lys Lys Arg Lys Ser Pro Gly Val Ala Ala Ala Val
 1 5 10 15
 Ala Glu Asp Gly Gly Leu Lys Lys Cys Lys Ile Ser Ser Tyr Cys Arg
 20 25 30
 Ser Gln Pro Pro Ala Arg Leu Ile Ser Gly Glu Glu His Phe Ser Ser
 35 40 45
 Lys Lys Cys Leu Ala Trp Phe Tyr Glu Tyr Ala Gly Pro Asp Glu Val
 50 55 60
 Val Gly Pro Glu Gly Met Glu Lys Phe Cys Glu Asp Ile Gly Val Glu
 65 70 75 80
 Pro Glu Asn Ile Ile Met Leu Val Leu Ala Trp Lys Leu Glu Ala Glu
 85 90 95
 Ser Met Gly Phe Phe Thr Lys Glu Glu Trp Leu Lys Gly Met Thr Ser

acc cac ccc gga gac ccc cgc ttc cag tgc agt ctc tgg cat ctc tat 462
 Thr His Pro Gly Asp Pro Arg Phe Gln Cys Ser Leu Trp His Leu Tyr
 90 95 100 105

ccc cta tga ggcaccacgt aagacctcct gcccttagct ctcttgctca 511
 Pro Leu

ccaccaaga acctcaggac agaagcgaga gccattgct cctgctcagc tcagcccggc 571

tgcgaggagaa cccttggcag gcagaacctg gaggtgtcag aggctcaact cctccatcta 631

accagcaggc tcccagagtc cccggaagag cctgcgcagc tgaagcagag tgcttctaga 691

tgagagagtgg tctactgggga aaaggacctg gccatcacct tccaatacct gctgcctgtc 751

tccctgaccc atgatctggc aagttaggca cagtcagaca tggacagttg atccatgagg 811

aaaagatgct ctccaccta aggccaggaa tctgagagca ggactggctg agctcccagg 871

gcaaggggtt cactaatgct tatcaataaa gaatattgag cctgg 916

<210> 120
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 120
 Met Gly Arg Lys Arg Leu Ile Thr Asp Ser Tyr Pro Val Val Lys Arg
 1 5 10 15
 Arg Glu Gly Pro Ala Gly His Ser Lys Gly Glu Leu Ala Pro Glu Leu
 20 25 30
 Gly Glu Glu Pro Gln Pro Arg Asp Glu Glu Glu Ala Glu Leu Glu Leu
 35 40 45
 Leu Arg Gln Phe Asp Leu Ala Trp Gln Tyr Gly Pro Cys Thr Gly Ile
 50 55 60
 Thr Arg Leu Gln Arg Trp Cys Arg Ala Lys Gln Met Gly Leu Glu Pro
 65 70 75 80
 Pro Pro Glu Val Trp Gln Val Leu Lys Thr His Pro Gly Asp Pro Arg
 85 90 95
 Phe Gln Cys Ser Leu Trp His Leu Tyr Pro Leu
 100 105

<210> 121
 <211> 1002
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (51)..(731)

<400> 121
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 Met Arg

cag aag cac tac ctt gag gct gca gcg cgg gga ctg cac gac agc tgc	104
Gln Lys His Tyr Leu Glu Ala Ala Arg Gly Leu His Asp Ser Cys	
5 10 15	
ccg ggc caa gcc cgc tac ctc ctt ctc ttt ctc ttt tac agc tgg gcc	152
Pro Gly Gln Ala Arg Tyr Leu Leu Leu Phe Leu Phe Tyr Ser Trp Ala	
20 25 30	
tac act tcg tcg cac gat gat aag agc act ttt gaa gaa acg tgt cca	200
Tyr Thr Ser Ser His Asp Asp Lys Ser Thr Phe Glu Glu Thr Cys Pro	
35 40 45 50	
tac tgt ttc cag ctg ttg gtt ctg gat aac tct cga gtg cgt ctc aaa	248
Tyr Cys Phe Gln Leu Leu Val Leu Asp Asn Ser Arg Val Arg Leu Lys	
55 60 65	
ccc aaa gcc agg ttg aca ccc aaa ata cag aaa ctt ctt aat cga gaa	296
Pro Lys Ala Arg Leu Thr Pro Lys Ile Gln Lys Leu Leu Asn Arg Glu	
70 75 80	
gcg aga aac tat aca ctc agt ttt aaa gaa gca aaa atg gtg aaa aag	344
Ala Arg Asn Tyr Thr Leu Ser Phe Lys Glu Ala Lys Met Val Lys Lys	
85 90 95	
ttc aaa gac tcc aaa agt gta ttg ttg atc act tgt aaa aca tgc aac	392
Phe Lys Asp Ser Lys Ser Val Leu Leu Ile Thr Cys Lys Thr Cys Asn	
100 105 110	
aga aca gtg aaa cat cat ggt aaa agt aga agc ttt gtg tca aca ttg	440
Arg Thr Val Lys His His Gly Lys Ser Arg Ser Phe Val Ser Thr Leu	
115 120 125 130	
aag agc aat cct gcc act cct aca agt aaa ctc agc ctg aag aca cca	488
Lys Ser Asn Pro Ala Thr Pro Thr Ser Lys Leu Ser Leu Lys Thr Pro	
135 140 145	
gag aga agg act gca aac cca aat cat gac atg tct ggc tcg aaa ggc	536
Glu Arg Arg Thr Ala Asn Pro Asn His Asp Met Ser Gly Ser Lys Gly	
150 155 160	
aag agc cca gca tcg gtt ttc aga aca cct aca tct gga cag tca gta	584
Lys Ser Pro Ala Ser Val Phe Arg Thr Pro Thr Ser Gly Gln Ser Val	
165 170 175	
tct act tgc tcc tca aag aac acc agc aaa aca aag aaa cac ttc tct	632
Ser Thr Cys Ser Ser Lys Asn Thr Ser Lys Thr Lys Lys His Phe Ser	
180 185 190	
caa cta aaa atg tta ctt agt cag aat gaa tcc caa aag att cca aag	680
Gln Leu Lys Met Leu Leu Ser Gln Asn Glu Ser Gln Lys Ile Pro Lys	
195 200 205 210	
gtg gac ttc aga aat ttc tta tct tct ctg aag ggt gga ctt tta aaa	728
Val Asp Phe Arg Asn Phe Leu Ser Ser Leu Lys Gly Gly Leu Leu Lys	
215 220 225	

taa gaaatgcctg atgtcaattc tgaaactaaa gttggtaaaa caacttttta 781

aactcttatt ctttttttga atacatggaa actagatctg aatgcaaact tttcttggca 841

tccttcagtg tttatgggga aaatacctca ttagtgtgaa tacctgaaac ctgcctacct 901

cataggacag ctgtgaggat caaaaaatat atgaaagttc cttgtagata catatctata 961

gatatatatg tgtatgtata taaagataga tatatacatt g 1002

<210> 122
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 122

Met	Arg	Gln	Lys	His	Tyr	Leu	Glu	Ala	Ala	Ala	Arg	Gly	Leu	His	Asp
1				5					10					15	
Ser	Cys	Pro	Gly	Gln	Ala	Arg	Tyr	Leu	Leu	Leu	Phe	Leu	Phe	Tyr	Ser
			20					25					30		
Trp	Ala	Tyr	Thr	Ser	Ser	His	Asp	Asp	Lys	Ser	Thr	Phe	Glu	Glu	Thr
			35				40					45			
Cys	Pro	Tyr	Cys	Phe	Gln	Leu	Leu	Val	Leu	Asp	Asn	Ser	Arg	Val	Arg
	50					55				60					
Leu	Lys	Pro	Lys	Ala	Arg	Leu	Thr	Pro	Lys	Ile	Gln	Lys	Leu	Leu	Asn
65					70					75					80
Arg	Glu	Ala	Arg	Asn	Tyr	Thr	Leu	Ser	Phe	Lys	Glu	Ala	Lys	Met	Val
				85					90					95	
Lys	Lys	Phe	Lys	Asp	Ser	Lys	Ser	Val	Leu	Leu	Ile	Thr	Cys	Lys	Thr
			100					105					110		
Cys	Asn	Arg	Thr	Val	Lys	His	His	Gly	Lys	Ser	Arg	Ser	Phe	Val	Ser
			115				120					125			
Thr	Leu	Lys	Ser	Asn	Pro	Ala	Thr	Pro	Thr	Ser	Lys	Leu	Ser	Leu	Lys
	130					135					140				
Thr	Pro	Glu	Arg	Arg	Thr	Ala	Asn	Pro	Asn	His	Asp	Met	Ser	Gly	Ser
145					150					155				160	
Lys	Gly	Lys	Ser	Pro	Ala	Ser	Val	Phe	Arg	Thr	Pro	Thr	Ser	Gly	Gln
				165				170						175	
Ser	Val	Ser	Thr	Cys	Ser	Ser	Lys	Asn	Thr	Ser	Lys	Thr	Lys	Lys	His
			180				185					190			
Phe	Ser	Gln	Leu	Lys	Met	Leu	Leu	Ser	Gln	Asn	Glu	Ser	Gln	Lys	Ile
	195					200					205				
Pro	Lys	Val	Asp	Phe	Arg	Asn	Phe	Leu	Ser	Ser	Leu	Lys	Gly	Gly	Leu
	210					215					220				
Leu	Lys														
225															

<210> 123
 <211> 1753
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (268)..(1455)

<400> 123

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cattcaggag tcctgtgctc cagtcacagc cttttctggt cttcagctag gagacaccaa 120

accctcagga agatttacta tagctaagag aaaactgcag cagaaagggc gcggctacct 180

acttcttaaa ttccgtttgt ggaccctcag actcttagtc ccctactccc agatacagcg 240

gccctaccgt ggctcctggc aagaagc atg gat ctc gga atc cct gac ctg ctg 294

Met Asp Leu Gly Ile Pro Asp Leu Leu

1

5

gac gcg tgg ctg gag ccc cca gag gat atc ttc tcg aca gga tcc gtc 342

Asp Ala Trp Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val

10

15

20

25

ctg gag ctg gga ctc cac tgc ccc cct cca gag gtt ccg gta act agg 390

Leu Glu Leu Gly Leu His Cys Pro Pro Pro Glu Val Pro Val Thr Arg

30

35

40

cta cag gaa cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc 438

Leu Gln Glu Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly

45

50

55

tgt ggc ctt caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att 486

Cys Gly Leu Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile

60

65

70

gat ccc aat gag gtg tac tgc tca gaa gca tct cct ggc agt gac agt 534

Asp Pro Asn Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser

75

80

85

ggc atc tct gag gac ccc tgc cat cca gac agt ccc cct gcc ccc agg 582

Gly Ile Ser Glu Asp Pro Cys His Pro Asp Ser Pro Pro Ala Pro Arg

90

95

100

105

gca acc agt tct cct atg ctc tat gag gtt gtc tat gag gca ggg gcc 630

Ala Thr Ser Ser Pro Met Leu Tyr Glu Val Val Tyr Glu Ala Gly Ala

110

115

120

ctg gag agg atg cag ggg gaa act ggg cca aat gta ggc ctt atc tcc 678

Leu Glu Arg Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser

125

130

135

atc cag cta gat cag tgg agc cca gca ttt atg gtg cct gat tcc tgc 726

Ile Gln Leu Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys

140

145

150

atg gtc agt gag ctg ccc ttt gat gct cat gcc cac atc ctg ccc aga 774

Met Val Ser Glu Leu Pro Phe Asp Ala His Ala His Ile Leu Pro Arg

155

160

165

gca ggc acc gta gcc cca gtg ccc tgt aca acc ctg ctg ccc tgt caa 822

Ala 170	Gly	Thr	Val	Ala	Pro	Val	Pro	Cys	Thr	Thr	Leu	Leu	Pro	Cys	Gln	185
acc Thr	ctg Leu	ttc Phe	ctg Leu	acc Thr	gat Asp	gag Glu	gag Glu	aag Lys	cgt Arg	ctg Leu	ctg Leu	ggg Gly	cag Gln	gaa Glu	ggg Gly	870
gtt Val	tcc Ser	ctg Leu	ccc Pro	tct Ser	cac His	ctg Leu	ccc Pro	ctc Leu	acc Thr	aag Lys	gca Ala	gag Glu	gag Glu	agg Arg	gtc Val	918
ctc Leu	aag Lys	aag Lys	gtc Val	agg Arg	agg Arg	aaa Lys	atc Ile	cgt Arg	aac Asn	aag Lys	cag Gln	tca Ser	gct Ala	cag Gln	gac Asp	966
agt Ser	cgg Arg	cgg Arg	cgg Arg	aag Lys	aag Lys	gag Glu	tac Tyr	att Ile	gat Asp	ggg Gly	ctg Leu	gag Glu	agc Ser	agg Arg	gtg Val	1014
gca Ala	gcc Ala	tgt Cys	tct Ser	gca Ala	cag Gln	aac Asn	caa Gln	gaa Glu	tta Leu	cag Gln	aaa Lys	aaa Lys	gtc Val	cag Gln	gag Glu	1062
ctg Leu	gag Glu	agg Arg	cac His	aac Asn	atc Ile	tcc Ser	ttg Leu	gta Val	gct Ala	cag Gln	ctc Leu	cgc Arg	cag Gln	ctg Leu	cag Gln	1110
acg Thr	cta Leu	att Ile	gct Ala	caa Gln	act Thr	tcc Ser	aac Asn	aaa Lys	gct Ala	gcc Ala	cag Gln	acc Thr	agc Ser	act Thr	tgt Cys	1158
gtt Val	ttg Leu	att Ile	ctt Leu	ctt Leu	ttt Phe	tcc Ser	ctg Leu	gct Ala	ctc Leu	atc Ile	atc Ile	ctg Leu	ccc Pro	agc Ser	ttc Phe	1206
agt Ser	cca Pro	ttc Phe	cag Gln	agt Ser	cga Arg	cca Pro	gaa Glu	gct Ala	ggg Gly	tct Ser	gag Glu	gat Asp	tac Tyr	cag Gln	cct Pro	1254
cac His	gga Gly	gtg Val	act Thr	tcc Ser	aga Arg	aat Asn	atc Ile	ctg Leu	acc Thr	cac His	aag Lys	gac Asp	gta Val	aca Thr	gaa Glu	1302
aat Asn	ctg Leu	gag Glu	acc Thr	caa Gln	gtg Val	gta Val	gag Glu	tcc Ser	aga Arg	ctg Leu	agg Arg	gag Glu	cca Pro	cct Pro	gga Gly	1350
gcc Ala	aag Lys	gat Asp	gca Ala	aat Asn	ggc Gly	tca Ser	aca Thr	agg Arg	aca Thr	ctg Leu	ctt Leu	gag Glu	aag Lys	atg Met	gga Gly	1398
ggg Gly	aag Lys	cca Pro	aga Arg	ccc Pro	agt Ser	ggg Gly	cgc Arg	atc Ile	cgg Arg	tcc Ser	gtg Val	ctg Leu	cat His	gca Ala	gat Asp	1446
gag atg tga gctggaacag accttcctgg cccacttcct gatcacaagg Glu Met																1495

395

aatcctgggc ttccttatgg ctttgcttcc cactgggatt cctacttagg tgtctgccct 1555
 caggggtcca aatcaacttca ggacacccca agagatgtcc tttagtctct gcctgaggcc 1615
 tagtctgcat ttgtttgcat atatgagagg gtacctcaaa tacttctgtt atgtatctgt 1675
 gattttatatt cttctttggg tatagggttg aggggaaata agttttgagt gagaaataaa 1735
 cgttttagct gaaattgt 1753

<210> 124
 <211> 395
 <212> PRT
 <213> Homo sapiens

<400> 124
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 Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu Gly Leu His Cys
 20 25 30
 Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln
 35 40 45
 Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu
 50 55 60
 Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys
 65 70 75 80
 Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Pro Cys
 85 90 95
 His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu
 100 105 110
 Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu
 115 120 125
 Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser
 130 135 140
 Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe
 145 150 155 160
 Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val
 165 170 175
 Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu
 180 185 190
 Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu
 195 200 205
 Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys Val Arg Arg Lys
 210 215 220
 Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg Arg Lys Lys Glu
 225 230 235 240
 Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys Ser Ala Gln Asn
 245 250 255
 Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg His Asn Ile Ser
 260 265 270
 Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile Ala Gln Thr Ser
 275 280 285
 Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile Leu Leu Phe Ser
 290 295 300

Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe Gln Ser Arg Pro
 305 310 315 320
 Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val Thr Ser Arg Asn
 325 330 335
 Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu Thr Gln Val Val
 340 345 350
 Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp Ala Asn Gly Ser
 355 360 365
 Thr Arg Thr Leu Leu Glu Lys Met Gly Gly Lys Pro Arg Pro Ser Gly
 370 375 380
 Arg Ile Arg Ser Val Leu His Ala Asp Glu Met
 385 390 395

<210> 125
 <211> 668
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (54)..(122)

<400> 125
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 Met
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gcg cct ggc tgt ggc cgc gtg gtc tct cac gca ggg gcg ccg ggc ggg 104
 Ala Pro Gly Cys Gly Arg Val Val Ser His Ala Gly Ala Pro Gly Gly
 5 10 15

gga acg cgg cca ccc tga gtctggtgag tcgactgcgg cggcctgtgt 152
 Gly Thr Arg Pro Pro
 20

ccgaagtgtc cggggccgtg aacaagggca gcggcctggc ctcaggcctg cgttcccacg 212
 tttggaaaacg gggagcttcg tcgattttgt ttacatcatc gactatgccca gggagttctc 272
 cagataagcc tggttttatt ttcgtcagtg aaaaggcctt accgtataac tgactttatg 332
 cttgccctgc ccccgataaa aataacttaa aagcagcgtg cctggttaca gctgtttcca 392
 cgtgcggtgc tcgtcgggag tgatcaccta ccctacaggt ggaagatgga tgcctgaagt 452
 gtagactgct gctagctgaa taccatctgg gagcataaag gtgacctgaa ggatgtcctt 512
 ggtgaggatt ttgaaaattt gatcttcaca agagttgcct ggatcatttg aaatttctgg 572
 gagtctgagg agtactgaca taattacctg ctggagtctg taaatacaca ttttaagacag 632
 tgaggatgtg aataaatata ttaatgcaaa aaaaac 668

<210> 126
 <211> 22

<212> PRT
<213> Homo sapiens

<400> 126
Met Ala Pro Gly Cys Gly Arg Val Val Ser His Ala Gly Ala Pro Gly
1 5 10 15
Gly Gly Thr Arg Pro Pro
20

<210> 127
<211> 279
<212> DNA
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<220>
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<222> (27)..(239)

<400> 127
atccctctcc acgacctcgg tcgagc atg ttc acc agg gcc cag gtg aga cgg 53
Met Phe Thr Arg Ala Gln Val Arg Arg
1 5

att ctg cag cgg gtg ccc ggg aag cag cga ttt ggc atc tac cgg ttc 101
Ile Leu Gln Arg Val Pro Gly Lys Gln Arg Phe Gly Ile Tyr Arg Phe
10 15 20 25

ctg ccc ttc ttt ttt gtc ctg gga gga acg atg gag tgg atc atg att 149
Leu Pro Phe Phe Phe Val Leu Gly Gly Thr Met Glu Trp Ile Met Ile
30 35 40

aaa gtg cgc gtg ggc cag gag acc ttc tat gat gtc tac cgt aga aaa 197
Lys Val Arg Val Gly Gln Glu Thr Phe Tyr Asp Val Tyr Arg Arg Lys
45 50 55

gcc tca gaa aga cag tat cag aga agg ctg gaa gat gaa tga 239
Ala Ser Glu Arg Gln Tyr Gln Arg Arg Leu Glu Asp Glu
60 65 70

gactgaactt cagcagtcaa taaagtcaat atgaattttt 279

<210> 128
<211> 70
<212> PRT
<213> Homo sapiens

<400> 128
Met Phe Thr Arg Ala Gln Val Arg Arg Ile Leu Gln Arg Val Pro Gly
1 5 10 15
Lys Gln Arg Phe Gly Ile Tyr Arg Phe Leu Pro Phe Phe Phe Val Leu
20 25 30
Gly Gly Thr Met Glu Trp Ile Met Ile Lys Val Arg Val Gly Gln Glu
35 40 45
Thr Phe Tyr Asp Val Tyr Arg Arg Lys Ala Ser Glu Arg Gln Tyr Gln
50 55 60

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<220>
<221> CDS
<222> (91)..(2178)
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140

Asn Phe Ile Gln Lys Asn Ser Met Asp Lys Lys Asn Gly Lys Ser Tyr	
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Glu Asn Lys Ser Gly Glu Asn Gln Ser Val Asp Lys Ser Asp Thr Ile	
170 175 180	
cca att cca aat ggt gtg gta aca aat aat tct ggt tat att act aat	690
Pro Ile Pro Asn Gly Val Val Thr Asn Asn Ser Gly Tyr Ile Thr Asn	
185 190 195 200	
ggt tat atg agt aaa gga gca gat aat gat ggt agt gga tct gag agc	738
Gly Tyr Met Ser Lys Gly Ala Asp Asn Asp Gly Ser Gly Ser Glu Ser	
205 210 215	
gga tat aca act cct aaa aaa agg aaa gct agg cgc aat agt gcc aag	786
Gly Tyr Thr Thr Pro Lys Lys Arg Lys Ala Arg Arg Asn Ser Ala Lys	
220 225 230	
ggt tgt gaa aac ctt aat ata gtg cag gac aaa ata atg caa caa gag	834
Gly Cys Glu Asn Leu Asn Ile Val Gln Asp Lys Ile Met Gln Gln Glu	
235 240 245	
acc agt gtc cca acc tta aaa cag gga ctt gaa act ttc aag cct gac	882
Thr Ser Val Pro Thr Leu Lys Gln Gly Leu Glu Thr Phe Lys Pro Asp	
250 255 260	
tat agt gaa caa aag gga aat cga gta gat ggt tcg aag ccc att tgg	930
Tyr Ser Glu Gln Lys Gly Asn Arg Val Asp Gly Ser Lys Pro Ile Trp	
265 270 275 280	
aag tat gaa act ggg cct gga gga aca agt cga gga aaa cct gct gtg	978
Lys Tyr Glu Thr Gly Pro Gly Gly Thr Ser Arg Gly Lys Pro Ala Val	
285 290 295	
ggt gat atg ctt cgg aaa agc tca gat agt aaa cct ggt gtg agc agc	1026
Gly Asp Met Leu Arg Lys Ser Ser Asp Ser Lys Pro Gly Val Ser Ser	
300 305 310	
aaa aag ttt gat gat cgg ccc aaa gga aag cat gct tca gct gtt gcc	1074
Lys Lys Phe Asp Asp Arg Pro Lys Gly Lys His Ala Ser Ala Val Ala	
315 320 325	
tcc aaa gag gac tcg tgg acc cta ttt aaa cca ccc cca gtt ttt cca	1122
Ser Lys Glu Asp Ser Trp Thr Leu Phe Lys Pro Pro Pro Val Phe Pro	
330 335 340	
gtg gac aat agc agt gct aaa ata gtt cct aaa ata agt tat gca agc	1170
Val Asp Asn Ser Ser Ala Lys Ile Val Pro Lys Ile Ser Tyr Ala Ser	
345 350 355 360	
aaa gtt aag gaa aac ctc aac aaa act ata cag aac tct tct gtg tca	1218
Lys Val Lys Glu Asn Leu Asn Lys Thr Ile Gln Asn Ser Ser Val Ser	
365 370 375	
cca act tca tct tca tca tct tca tca tct acc ggg gaa act cag acc	1266
Pro Thr Ser Ser Ser Ser Ser Ser Ser Ser Thr Gly Glu Thr Gln Thr	

380	385	390	
caa tca tca agt cgc tta tcc cag gtc cct atg tca gcg ctg aaa tct Gln Ser Ser Ser Arg Leu Ser Gln Val Pro Met Ser Ala Leu Lys Ser 395 400 405			1314
gtt act tct gcc aac ttt tct aat ggg cct gtt tta gca ggg act gat Val Thr Ser Ala Asn Phe Ser Asn Gly Pro Val Leu Ala Gly Thr Asp 410 415 420			1362
gga aat gtt tat cct cca ggg ggt cag cca ctg cta act act gct gct Gly Asn Val Tyr Pro Pro Gly Gly Gln Pro Leu Leu Thr Thr Ala Ala 425 430 435 440			1410
aat act cta aca ccc atc tct tct ggg aca gat tca gtt ctc cag gac Asn Thr Leu Thr Pro Ile Ser Ser Gly Thr Asp Ser Val Leu Gln Asp 445 450 455			1458
atg agt cta act tca gca gct gtt gaa caa att aag act agc ctt ttt Met Ser Leu Thr Ser Ala Ala Val Glu Gln Ile Lys Thr Ser Leu Phe 460 465 470			1506
atc tat cct tca aat atg caa act atg ctg ttg agc aca gca caa gtg Ile Tyr Pro Ser Asn Met Gln Thr Met Leu Leu Ser Thr Ala Gln Val 475 480 485			1554
gat ctg ccc tct cag aca gat cag caa aac ctg ggg gat atc ttc cag Asp Leu Pro Ser Gln Thr Asp Gln Gln Asn Leu Gly Asp Ile Phe Gln 490 495 500			1602
aat cag tgg ggt tta tca ttt ata aat gag ccc agt gct ggc cct gag Asn Gln Trp Gly Leu Ser Phe Ile Asn Glu Pro Ser Ala Gly Pro Glu 505 510 515 520			1650
act gtt act ggg aag tca tca gag cat aaa gtg atg gag gtg aca ttt Thr Val Thr Gly Lys Ser Ser Glu His Lys Val Met Glu Val Thr Phe 525 530 535			1698
caa gga gaa tat cct gct act ttg gtt tca cag ggt gct gaa ata att Gln Gly Glu Tyr Pro Ala Thr Leu Val Ser Gln Gly Ala Glu Ile Ile 540 545 550			1746
ccc tca gga act gag cat cct gtg ttt ccc aag gct tac gag ctg gag Pro Ser Gly Thr Glu His Pro Val Phe Pro Lys Ala Tyr Glu Leu Glu 555 560 565			1794
aaa cgg act agt cct caa gtt ctg ggt agc att cta aaa tct ggg act Lys Arg Thr Ser Pro Gln Val Leu Gly Ser Ile Leu Lys Ser Gly Thr 570 575 580			1842
act agt gag agt gga gcc tta tcc ttg gaa ccc agt cat ata ggt gac Thr Ser Glu Ser Gly Ala Leu Ser Leu Glu Pro Ser His Ile Gly Asp 585 590 595 600			1890
ctg cag aaa gca gac acc agt agt caa ggt gct tta gtg ttt ctc tca Leu Gln Lys Ala Asp Thr Ser Ser Gln Gly Ala Leu Val Phe Leu Ser 605 610 615			1938

aag gac tac gag ata gaa agt caa aat cct ctg gcc tct cct acg aac 1986
 Lys Asp Tyr Glu Ile Glu Ser Gln Asn Pro Leu Ala Ser Pro Thr Asn
 620 625 630

act ttg tta ggc tct gcc aaa gaa cag aga tac cag aga ggc cta gaa 2034
 Thr Leu Leu Gly Ser Ala Lys Glu Gln Arg Tyr Gln Arg Gly Leu Glu
 635 640 645

agg aat gat agc tgg ggt tct ttt gac ctg agg gct gct att gta tat 2082
 Arg Asn Asp Ser Trp Gly Ser Phe Asp Leu Arg Ala Ala Ile Val Tyr
 650 655 660

cac act aaa gaa atg gaa tct att tgg aat ttg cag aag caa gat ccc 2130
 His Thr Lys Glu Met Glu Ser Ile Trp Asn Leu Gln Lys Gln Asp Pro
 665 670 675 680

aaa agg ata atc act tac aat gaa gcc atg gat agt cca gat caa tga 2178
 Lys Arg Ile Ile Thr Tyr Asn Glu Ala Met Asp Ser Pro Asp Gln
 685 690 695

aggaccagac tgcctattcg taacctttct gcagcattag agccatcggt catgggggac 2238

acaaggcttt tatgctccta gatcttcaac gcagcagagg aaccataagt agaatacacag 2298

gataatatat acaaatatat atatatacat atatatatat atagttattt aaaaaaggca 2358

actgaaagta attagacttc ttaaggaatc aaatttattt caagagacta cacatgggta 2418

tttaatctcc ggtactgaat aggttttttt tcttctgtta gtttttggtt ttaagtgtga 2478

atgcaagtga ttaatgaata cagacttaac aagtgtgggt ctaaagttcc tgctgtcatc 2538

aacttgggca acaaatgacc cactggaaag gcaaatccac ttaaaagatc tctgtatcct 2598

gttctgtgac tgaagtata cactaatcac ggggaaccca gaatgattca acattttccc 2658

cccactctc ccttgatctt tttgggttta cttaattaa gccctgagag aatgctggat 2718

aaatgccttg aagttagcag ggtgtatttt tttagcgaat atgatttgca tgtcttgcca 2778

ggagttaagc ggcctctggg gtgttgggga aatactttat ttctttccat ttattttttg 2838

tggggcgggg ataggggagg gcattgaagt tctacaattc tggaatagtt agttgatgg 2898

acatagttaa cttggcttcg gttacatatt ggactttaac aactgaagaa tctatgcgtg 2958

tcattttaaag aaaagttgca gaacaagcaa ttggcttaga tatacaatct ggaaaaatat 3018

tcctgtgccc atattttaat gtaattgtat aactgggagc aaaaatatat tctgcttttc 3078

aactgtaggt gctccagact tgctctccgt cactaacact aaatgtgctg ttttcttctg 3138

ttttcatcaa acatttaaga caaacttaga ctttctgtta aattatcttt taatttctca 3198

gcaaaatcta aaaggggaag aaaaaagtcc atgaaaacta aaacttttca tgtttttagc 3258

cagtgagaag ataataaacc ctgactgtag aagggtgtgtt ttcatgcaaa ctatacttct 3318

gagcttggtta gcttctaatt atatcttaat aaatatattt tattactag 3367

<210> 130

<211> 695

<212> PRT

<213> Homo sapiens

<400> 130

Met	Glu	Glu	Lys	Pro	Gly	Gln	Pro	Gln	Pro	Gln	His	His	His	Ser	His
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His	His	Pro	His	His	His	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Pro	His	His
			20					25					30		
His	His	His	Tyr	Tyr	Phe	Tyr	Asn	His	Ser	His	Asn	His	His	His	His
			35				40					45			
His	His	His	Gln	Gln	Pro	His	Gln	Tyr	Leu	Gln	His	Gly	Ala	Glu	Gly
			50				55				60				
Ser	Pro	Lys	Ala	Gln	Pro	Lys	Pro	Leu	Lys	His	Glu	Gln	Lys	His	Thr
65					70					75					80
Leu	Gln	Gln	His	Gln	Glu	Thr	Pro	Lys	Lys	Lys	Thr	Gly	Tyr	Gly	Glu
				85					90					95	
Leu	Asn	Gly	Asn	Ala	Gly	Glu	Arg	Glu	Ile	Ser	Leu	Lys	Asn	Leu	Ser
			100					105					110		
Ser	Asp	Glu	Ala	Thr	Asn	Pro	Ile	Ser	Arg	Val	Leu	Asn	Gly	Asn	Gln
			115				120						125		
Gln	Val	Val	Asp	Thr	Ser	Leu	Lys	Gln	Thr	Val	Lys	Ala	Asn	Thr	Phe
			130				135					140			
Gly	Lys	Ala	Gly	Ile	Lys	Thr	Lys	Asn	Phe	Ile	Gln	Lys	Asn	Ser	Met
145					150				155						160
Asp	Lys	Lys	Asn	Gly	Lys	Ser	Tyr	Glu	Asn	Lys	Ser	Gly	Glu	Asn	Gln
				165					170					175	
Ser	Val	Asp	Lys	Ser	Asp	Thr	Ile	Pro	Ile	Pro	Asn	Gly	Val	Val	Thr
			180					185					190		
Asn	Asn	Ser	Gly	Tyr	Ile	Thr	Asn	Gly	Tyr	Met	Ser	Lys	Gly	Ala	Asp
			195				200					205			
Asn	Asp	Gly	Ser	Gly	Ser	Glu	Ser	Gly	Tyr	Thr	Thr	Pro	Lys	Lys	Arg
			210				215					220			
Lys	Ala	Arg	Arg	Asn	Ser	Ala	Lys	Gly	Cys	Glu	Asn	Leu	Asn	Ile	Val
225					230					235					240
Gln	Asp	Lys	Ile	Met	Gln	Gln	Glu	Thr	Ser	Val	Pro	Thr	Leu	Lys	Gln
				245					250					255	
Gly	Leu	Glu	Thr	Phe	Lys	Pro	Asp	Tyr	Ser	Glu	Gln	Lys	Gly	Asn	Arg
			260					265					270		
Val	Asp	Gly	Ser	Lys	Pro	Ile	Trp	Lys	Tyr	Glu	Thr	Gly	Pro	Gly	Gly
			275				280						285		
Thr	Ser	Arg	Gly	Lys	Pro	Ala	Val	Gly	Asp	Met	Leu	Arg	Lys	Ser	Ser
			290				295				300				
Asp	Ser	Lys	Pro	Gly	Val	Ser	Ser	Lys	Lys	Phe	Asp	Asp	Arg	Pro	Lys
305					310					315					320
Gly	Lys	His	Ala	Ser	Ala	Val	Ala	Ser	Lys	Glu	Asp	Ser	Trp	Thr	Leu
				325					330					335	
Phe	Lys	Pro	Pro	Pro	Val	Phe	Pro	Val	Asp	Asn	Ser	Ser	Ala	Lys	Ile
			340					345					350		
Val	Pro	Lys	Ile	Ser	Tyr	Ala	Ser	Lys	Val	Lys	Glu	Asn	Leu	Asn	Lys
			355				360						365		

Thr	Ile	Gln	Asn	Ser	Ser	Val	Ser	Pro	Thr	Ser	Ser	Ser	Ser	Ser	Ser	
370						375				380						
Ser	Ser	Thr	Gly	Glu	Thr	Gln	Thr	Gln	Ser	Ser	Ser	Arg	Leu	Ser	Gln	
385					390				395						400	
Val	Pro	Met	Ser	Ala	Leu	Lys	Ser	Val	Thr	Ser	Ala	Asn	Phe	Ser	Asn	
			405						410					415		
Gly	Pro	Val	Leu	Ala	Gly	Thr	Asp	Gly	Asn	Val	Tyr	Pro	Pro	Gly	Gly	
		420						425					430			
Gln	Pro	Leu	Leu	Thr	Thr	Ala	Ala	Asn	Thr	Leu	Thr	Pro	Ile	Ser	Ser	
		435				440						445				
Gly	Thr	Asp	Ser	Val	Leu	Gln	Asp	Met	Ser	Leu	Thr	Ser	Ala	Ala	Val	
450						455						460				
Glu	Gln	Ile	Lys	Thr	Ser	Leu	Phe	Ile	Tyr	Pro	Ser	Asn	Met	Gln	Thr	
465					470					475					480	
Met	Leu	Leu	Ser	Thr	Ala	Gln	Val	Asp	Leu	Pro	Ser	Gln	Thr	Asp	Gln	
			485						490					495		
Gln	Asn	Leu	Gly	Asp	Ile	Phe	Gln	Asn	Gln	Trp	Gly	Leu	Ser	Phe	Ile	
		500						505					510			
Asn	Glu	Pro	Ser	Ala	Gly	Pro	Glu	Thr	Val	Thr	Gly	Lys	Ser	Ser	Glu	
		515					520					525				
His	Lys	Val	Met	Glu	Val	Thr	Phe	Gln	Gly	Glu	Tyr	Pro	Ala	Thr	Leu	
530						535						540				
Val	Ser	Gln	Gly	Ala	Glu	Ile	Ile	Pro	Ser	Gly	Thr	Glu	His	Pro	Val	
545					550					555					560	
Phe	Pro	Lys	Ala	Tyr	Glu	Leu	Glu	Lys	Arg	Thr	Ser	Pro	Gln	Val	Leu	
			565						570					575		
Gly	Ser	Ile	Leu	Lys	Ser	Gly	Thr	Thr	Ser	Glu	Ser	Gly	Ala	Leu	Ser	
		580						585					590			
Leu	Glu	Pro	Ser	His	Ile	Gly	Asp	Leu	Gln	Lys	Ala	Asp	Thr	Ser	Ser	
		595					600					605				
Gln	Gly	Ala	Leu	Val	Phe	Leu	Ser	Lys	Asp	Tyr	Glu	Ile	Glu	Ser	Gln	
610						615					620					
Asn	Pro	Leu	Ala	Ser	Pro	Thr	Asn	Thr	Leu	Leu	Gly	Ser	Ala	Lys	Glu	
625					630					635					640	
Gln	Arg	Tyr	Gln	Arg	Gly	Leu	Glu	Arg	Asn	Asp	Ser	Trp	Gly	Ser	Phe	
			645						650					655		
Asp	Leu	Arg	Ala	Ala	Ile	Val	Tyr	His	Thr	Lys	Glu	Met	Glu	Ser	Ile	
			660					665					670			
Trp	Asn	Leu	Gln	Lys	Gln	Asp	Pro	Lys	Arg	Ile	Ile	Thr	Tyr	Asn	Glu	
		675					680					685				
Ala	Met	Asp	Ser	Pro	Asp	Gln										
690						695										

<210> 131
 <211> 1290
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (100)..(699)

<400> 131
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 ttctcagccg ggccgcgcgac ccaaaggagc cgtccgact atg tct aac atg gag 114

	Met	Ser	Asn	Met	Glu	
	1				5	
aaa cac ctg ttc aac ctg aag ttc gcg gcc aaa gaa ctg agt agg agt						162
Lys His Leu Phe Asn Leu Lys Phe Ala Ala Lys Glu Leu Ser Arg Ser						
	10			15	20	
gcc aaa aaa tgc gat aag gag gaa aag gcc gaa aag gcc aaa att aaa						210
Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala Glu Lys Ala Lys Ile Lys						
	25			30	35	
aag gcc att cag aag ggc aac atg gaa gtt gcg agg ata cac gcc gaa						258
Lys Ala Ile Gln Lys Gly Asn Met Glu Val Ala Arg Ile His Ala Glu						
	40			45	50	
aat gcc atc cgc cag aag aac cag gcg gtg aat ttc ttg aga atg agt						306
Asn Ala Ile Arg Gln Lys Asn Gln Ala Val Asn Phe Leu Arg Met Ser						
	55			60	65	
gcg cga gtc gat gca gtg gct gcc agg gtc cag acg gcg gtg acg atg						354
Ala Arg Val Asp Ala Val Ala Ala Arg Val Gln Thr Ala Val Thr Met						
	70			75	80	85
ggc aag gtg acc aag tcg atg gct ggt gtg gtt aag tcg atg gat gcg						402
Gly Lys Val Thr Lys Ser Met Ala Gly Val Val Lys Ser Met Asp Ala						
	90			95	100	
aca ttg aag acc atg aat ctg gag aag att tct gct ttg atg gac aaa						450
Thr Leu Lys Thr Met Asn Leu Glu Lys Ile Ser Ala Leu Met Asp Lys						
	105			110	115	
ttc gag cac cag ttt gag act ctg gac gtc cag acg cag caa atg gaa						498
Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln Thr Gln Gln Met Glu						
	120			125	130	
gac acg atg agc agc acg acg acg ctc acc act ccc cag aac caa gtg						546
Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr Pro Gln Asn Gln Val						
	135			140	145	
gat atg ctg ctc cag gaa atg gca gat gag gcg ggc ctc gac ctc aac						594
Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala Gly Leu Asp Leu Asn						
	150			155	160	165
atg gag ctg ccg cag ggc cag acc ggc tcc gtg ggc acg agc gtg gct						642
Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val Gly Thr Ser Val Ala						
	170			175	180	
tcg gcg gag cag gat gaa ctg tct cag aga ctg gcc cgc ctt cgg gat						690
Ser Ala Glu Gln Asp Glu Leu Ser Gln Arg Leu Ala Arg Leu Arg Asp						
	185			190	195	
caa gtg tga cggcagaacc cgctctgagg tttcctggcc atagccaccc						739
Gln Val						
tttgaaatgc tctctgtgtg ttagagagat actataccct agaaactctg aacacgccag						799
aatgctgaaa tgcccttcta cctttgggtt tacagccccc tccacataaa ttaagaaatt						859

cagtatttct gcactcttag ctggattcta aagttctgta tagctcgtaa tgatgggtatt 919
 tttatagcag ccttttaaca gaactagtta atttcgtgta tatgaatctt tctcgaagat 979
 ctgggtcaaaa ctgtattcag tttcctgccc agaatgatca gattgaaggt ggttggtttt 1039
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 agaggggaaa gattacttag tttggttata cagttataaa caccatgcag tgtattcgggt 1159
 ggactgtgct atttctgttt atcctttggg ttttggtttt tgtttttttt ttttgccttc 1219
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 atttatactg g 1290

<210> 132
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 132
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 Glu Leu Ser Arg Ser Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala Glu
 20 25 30
 Lys Ala Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Met Glu Val Ala
 35 40 45
 Arg Ile His Ala Glu Asn Ala Ile Arg Gln Lys Asn Gln Ala Val Asn
 50 55 60
 Phe Leu Arg Met Ser Ala Arg Val Asp Ala Val Ala Ala Arg Val Gln
 65 70 75 80
 Thr Ala Val Thr Met Gly Lys Val Thr Lys Ser Met Ala Gly Val Val
 85 90 95
 Lys Ser Met Asp Ala Thr Leu Lys Thr Met Asn Leu Glu Lys Ile Ser
 100 105 110
 Ala Leu Met Asp Lys Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln
 115 120 125
 Thr Gln Gln Met Glu Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr
 130 135 140
 Pro Gln Asn Gln Val Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala
 145 150 155 160
 Gly Leu Asp Leu Asn Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val
 165 170 175
 Gly Thr Ser Val Ala Ser Ala Glu Gln Asp Glu Leu Ser Gln Arg Leu
 180 185 190
 Ala Arg Leu Arg Asp Gln Val
 195

<210> 133
 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (24)..(380)

<400> 133

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gacctgccggg agcttggtgc gct atg gcg aca ccc agc ctg cgg ggt cgt ctg 53
      Met Ala Thr Pro Ser Leu Arg Gly Arg Leu
      1              5              10

gcg cgg ttt ggg aac ccg cgg aag cct gtg ctg aag ccc aat aaa cct 101
Ala Arg Phe Gly Asn Pro Arg Lys Pro Val Leu Lys Pro Asn Lys Pro
      15              20              25

ctc att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag 149
Leu Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu
      30              35              40

gcg act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag 197
Ala Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln
      45              50              55

aat gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc 245
Asn Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu
      60              65              70

gat tgt gcc gcg agg gct cag gaa gcc cga aag atg aga tca ata cag 293
Asp Cys Ala Ala Arg Ala Gln Glu Ala Arg Lys Met Arg Ser Ile Gln
      75              80              85              90

gaa acc ctg gga gag tct ggg agt tta ctt cca aat aaa ttg aat aag 341
Glu Thr Leu Gly Glu Ser Gly Ser Leu Leu Pro Asn Lys Leu Asn Lys
      95              100              105

ttg tta cag agg ttt cct aac aaa cct tac ctc agc tga aaatggacaa 390
Leu Leu Gln Arg Phe Pro Asn Lys Pro Tyr Leu Ser
      110              115

gtattttcaa tgactgaaat atagcttctg acaactatgc agaggcattt tagagacatt 450

ggcattgccca tgccctcttt ggagggtaga agaggcaaaa cacttttttc acccttttga 510

atcatagtat gggtagaagt tatgatttat cttgaaataa aatcctctga acag 564

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<210> 134
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 134

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Met Ala Thr Pro Ser Leu Arg Gly Arg Leu Ala Arg Phe Gly Asn Pro
  1              5              10              15
Arg Lys Pro Val Leu Lys Pro Asn Lys Pro Leu Ile Leu Ala Asn Arg
      20              25              30
Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala Thr Cys Ile Thr Glu
      35              40              45
Met Ser Val Met Met Ala Cys Trp Lys Gln Asn Glu Phe Arg Asp Asp

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09890688-092704

WORLD BANK

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<221> CDS
<222> {467}..(811)
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cag ccc tgt gcc agg agg ctg gct gga ata aag gta cag ata gag gcc 523
Gln Pro Cys Ala Arg Arg Leu Ala Gly Ile Lys Val Gln Ile Glu Ala
5 10 15

ccc acc tgc ccc cag ggc cac agc tgc atc tcc tgc cct gct gtc att 619
Pro Thr Cys Pro Gln Gly His Ser Cys Ile Ser Cys Pro Ala Val Ile
40 45 50

tgt tgc tgt gta ttc ctg ccg gcc agg ggc cac tgc cag gac cac gcc 715
Cys Cys Cys Val Phe Leu Pro Ala Arg Gly His Cys Gln Asp His Ala

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70              75              80
tcc ctt ttc ata tcc cga ttc tta agt tct gct att gtg gta ttc tgg 763
Ser Leu Phe Ile Ser Arg Phe Leu Ser Ser Ala Ile Val Val Phe Trp
85              90              95

tgg aga aaa aag aac cgc gtg gct gtt ttt gaa ctg cct gga acc taa 811
Trp Arg Lys Lys Asn Arg Val Ala Val Phe Glu Leu Pro Gly Thr
100              105              110

gaccctgaat tcttttcccc cccaagggga aaatctatat ggaaaacatt tatttttaaaa 871

tacaggatga agtgaattaa aagatttaaa tgc 904

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<210> 136
 <211> 114
 <212> PRT
 <213> Homo sapiens

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<400> 136
Met Trp Ala Gln Pro Cys Ala Arg Arg Leu Ala Gly Ile Lys Val Gln
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Ile Glu Ala Ser Pro Pro Leu Gly Pro Leu Ala Leu Arg Val Phe Ala
20     25     30
Ala Ser Glu Pro Thr Cys Pro Gln Gly His Ser Cys Ile Ser Cys Pro
35     40     45
Ala Val Ile Thr Gly Met Gly Arg Leu Ala Trp Gly His Pro Leu Pro
50     55     60
Leu Pro Gly Cys Cys Cys Val Phe Leu Pro Ala Arg Gly His Cys Gln
65     70     75     80
Asp His Ala Ser Leu Phe Ile Ser Arg Phe Leu Ser Ser Ala Ile Val
85     90     95
Val Phe Trp Trp Arg Lys Lys Asn Arg Val Ala Val Phe Glu Leu Pro
100    105    110
Gly Thr

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<210> 137
 <211> 472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (90)..(353)

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<400> 137
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ctacagagtg aaggttttaa tccaagggtc atg gca aaa cat ctg aag ttc atc 113
Met Ala Lys His Leu Lys Phe Ile
1      5

gcc agg act gtg atg gta cag gaa ggg aac gtg gaa agc gca tac agg 161
Ala Arg Thr Val Met Val Gln Glu Gly Asn Val Glu Ser Ala Tyr Arg

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10              15              20
acc cta aac aga atc ctc act atg gat ggg ctc att gag gac att aag 209
Thr Leu Asn Arg Ile Leu Thr Met Asp Gly Leu Ile Glu Asp Ile Lys
25              30              35              40

cat cgg cgg tat tat gag aag cca tgc cgc cgg cga cag agg gaa agc 257
His Arg Arg Tyr Tyr Glu Lys Pro Cys Arg Arg Arg Gln Arg Glu Ser
45              50              55

tat gaa agg tgc cgg cgg atc tac aac atg gaa atg gct cgc aag atc 305
Tyr Glu Arg Cys Arg Arg Ile Tyr Asn Met Glu Met Ala Arg Lys Ile
60              65              70

aac ttc ttg atg cga aag aat cgg gca gat ccg tgg cag ggc tgc tga 353
Asn Phe Leu Met Arg Lys Asn Arg Ala Asp Pro Trp Gln Gly Cys
75              80              85

ggcctgtggg tgggacaccc agtgcgaaac cctcatccag ttttctctcc atctcttttc 413
tttgtacaat cccatttcct attaccattc tctgcaataa actcaaatca catgtctgc 472

<210> 138
<211> 87
<212> PRT
<213> Homo sapiens

<400> 138
Met Ala Lys His Leu Lys Phe Ile Ala Arg Thr Val Met Val Gln Glu
1              5              10              15
Gly Asn Val Glu Ser Ala Tyr Arg Thr Leu Asn Arg Ile Leu Thr Met
20              25              30
Asp Gly Leu Ile Glu Asp Ile Lys His Arg Arg Tyr Tyr Glu Lys Pro
35              40              45
Cys Arg Arg Arg Gln Arg Glu Ser Tyr Glu Arg Cys Arg Arg Ile Tyr
50              55              60
Asn Met Glu Met Ala Arg Lys Ile Asn Phe Leu Met Arg Lys Asn Arg
65              70              75              80
Ala Asp Pro Trp Gln Gly Cys
85

<210> 139
<211> 180
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (49)..(168)

<400> 139
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Met Gly Arg
1

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ggt ggg ggt ggg ggg gca gag gcg tct gac ccc agg aac ctg cag ggc 105
Gly Gly Gly Gly Gly Ala Glu Ala Ser Asp Pro Arg Asn Leu Gln Gly
5 10 15

ggg gct ggg tcg gtg ccc tct aag gac aat ttt gac ctt gtt caa cct 153
Gly Ala Gly Ser Val Pro Ser Lys Asp Asn Phe Asp Leu Val Gln Pro
20 25 30 35

ttc cac aaa gaa taa attgtgtttc ac 180
Phe His Lys Glu

<210> 140
<211> 39
<212> PRT
<213> Homo sapiens

<400> 140
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Val Gln Pro Phe His Lys Glu
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<210> 141
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (35)..(343)

<400> 141
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tgg cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg 103
Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg
10 15 20

ccg cgg ttc gtg tcg ttg cgc gcc aag cag aac atg atc cgc cgc ctg 151
Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu
25 30 35

gag atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc 199
Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr
40 45 50 55

cgg gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc 247
Arg Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe
60 65 70

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BOOKS

[illegible]

BOOKS

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BOOKS

BOOKS

BOOKS

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BOOK REVIEW

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BOOKS

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BOOKS

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BOOK REVIEW

[illegible]

agc gtc atc cag aac ctg ccc aag aac ggt tct tac cgc ccc tcc tat	213
Ser Val Ile Gln Asn Leu Pro Lys Asn Gly Ser Tyr Arg Pro Ser Tyr	
25 30 35	
gaa gag atg ctg cga ttc tac agt tac tac aag cag gcc acc atg ggg	261
Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln Ala Thr Met Gly	
40 45 50	
ccc tgc ctg gtc ccc cgg ccc ggg ttc tgg gac ccc att gga cga tat	309
Pro Cys Leu Val Pro Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg Tyr	
55 60 65	
aag tgg gac gcc tgg aac agt ctg ggc aag atg agc agg gag gag gcc	357
Lys Trp Asp Ala Trp Asn Ser Leu Gly Lys Met Ser Arg Glu Glu Ala	
70 75 80	
atg tct gcc tac atc act gaa atg aaa ctg gtg gca cag aag gtg atc	405
Met Ser Ala Tyr Ile Thr Glu Met Lys Leu Val Ala Gln Lys Val Ile	
85 90 95 100	
gac aca gtg ccc ctg ggt gag gtg gca gag gac atg ttt ggt tac ttc	453
Asp Thr Val Pro Leu Gly Glu Val Ala Glu Asp Met Phe Gly Tyr Phe	
105 110 115	
gag ccc ctg tac cag gtg atc cct gac atg ccg agg ccc cca gag acc	501
Glu Pro Leu Tyr Gln Val Ile Pro Asp Met Pro Arg Pro Pro Glu Thr	
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ttc ctg aga agg gtc aca ggt tgg aaa gag cag gtt gtg aat gga gat	549
Phe Leu Arg Arg Val Thr Gly Trp Lys Glu Gln Val Val Asn Gly Asp	
135 140 145	
gtt ggg gct gtt tca gag cct ccc tgc ctc ccc aag gaa ccg gca ccc	597
Val Gly Ala Val Ser Glu Pro Pro Cys Leu Pro Lys Glu Pro Ala Pro	
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cca agc cca gct tcc ctc tgg gca gta act cta cca acc cct cca cag	645
Pro Ser Pro Ala Ser Leu Trp Ala Val Thr Leu Pro Thr Pro Pro Gln	
165 170 175 180	
agt ccc att cac cca ggg acc tgg act ccg agg ttt tct gtg att ccc	693
Ser Pro Ile His Pro Gly Thr Trp Thr Pro Arg Phe Ser Val Ile Pro	
185 190 195	
tgg agc agc tgg agc ctg agc tgg ttt gga cag agc agc ggg cag cat	741
Trp Ser Ser Trp Ser Leu Ser Trp Phe Gly Gln Ser Ser Gly Gln His	
200 205 210	
ctg gag gaa agc gtg atc cca gga aca gcc ccg tgc ccc cca caa aga	789
Leu Glu Glu Ser Val Ile Pro Gly Thr Ala Pro Cys Pro Pro Gln Arg	
215 220 225	
aag agg ggt tgc ggg gca gcc cgc cgg ggc ccc agg agt tgg acg tgt	837
Lys Arg Gly Cys Gly Ala Ala Arg Arg Gly Pro Arg Ser Trp Thr Cys	
230 235 240	
ggc tgc tgg gga cag ttc gag cac tac agg aga gca tgc agg agg tgc	885

Gly Cys Trp Gly Gln Phe Glu His Tyr Arg Arg Ala Cys Arg Arg Cys
 245 250 255 260

agg cga ggg tgc aga gcc tgg aga gca tgc ccc ggc ccc ctg agc aga 933
 Arg Arg Gly Cys Arg Ala Trp Arg Ala Cys Pro Gly Pro Leu Ser Arg
 265 270 275

ggc cgc agc cca ggc cca gtg ctc ggc cat ggc ccc ttg ggc tcc cgg 981
 Gly Arg Ser Pro Gly Pro Val Leu Gly His Gly Pro Leu Gly Ser Arg
 280 285 290

ggc ccg cgc tgc tct tct tcc tcc tgt ggc cct tcg tcg tcc agt ggc 1029
 Gly Pro Arg Cys Ser Ser Ser Ser Cys Gly Pro Ser Ser Ser Ser Gly
 295 300 305

tct tcc gaa tgt ttc gga ccc aaa aga ggt gac tgt cag tgg agg ggt 1077
 Ser Ser Glu Cys Phe Gly Pro Lys Arg Gly Asp Cys Gln Trp Arg Gly
 310 315 320

ctc tgc agc caa ctg aga cta tct tgc tgt gcc ctg agc ctt cct agg 1125
 Leu Cys Ser Gln Leu Arg Leu Ser Cys Cys Ala Leu Ser Leu Pro Arg
 325 330 335 340

gtt tag aagaacagca ttcaaaattc cccgtcctgt cagtgtttgc cttcgcacct 1181
 Val

cctcccctaa agcagcgcgg ggggcaaata agaccccacc cctccctgca gcttcacagg 1241

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cag 1664

<210> 144
 <211> 341
 <212> PRT
 <213> Homo sapiens

<400> 144
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 Arg Pro Ser Tyr Glu Glu Met Leu Arg Phe Tyr Ser Tyr Tyr Lys Gln
 35 40 45

09890688-092701

Ala	Thr	Met	Gly	Pro	Cys	Leu	Val	Pro	Arg	Pro	Gly	Phe	Trp	Asp	Pro
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Arg	Glu	Glu	Ala	Met	Ser	Ala	Tyr	Ile	Thr	Glu	Met	Lys	Leu	Val	Ala
				85					90					95	
Gln	Lys	Val	Ile	Asp	Thr	Val	Pro	Leu	Gly	Glu	Val	Ala	Glu	Asp	Met
			100					105					110		
Phe	Gly	Tyr	Phe	Glu	Pro	Leu	Tyr	Gln	Val	Ile	Pro	Asp	Met	Pro	Arg
		115					120					125			
Pro	Pro	Glu	Thr	Phe	Leu	Arg	Arg	Val	Thr	Gly	Trp	Lys	Glu	Gln	Val
	130					135					140				
Val	Asn	Gly	Asp	Val	Gly	Ala	Val	Ser	Glu	Pro	Pro	Cys	Leu	Pro	Lys
145					150					155					160
Glu	Pro	Ala	Pro	Pro	Ser	Pro	Ala	Ser	Leu	Trp	Ala	Val	Thr	Leu	Pro
				165					170					175	
Thr	Pro	Pro	Gln	Ser	Pro	Ile	His	Pro	Gly	Thr	Trp	Thr	Pro	Arg	Phe
			180					185					190		
Ser	Val	Ile	Pro	Trp	Ser	Ser	Trp	Ser	Leu	Ser	Trp	Phe	Gly	Gln	Ser
		195					200					205			
Ser	Gly	Gln	His	Leu	Glu	Glu	Ser	Val	Ile	Pro	Gly	Thr	Ala	Pro	Cys
	210					215					220				
Pro	Pro	Gln	Arg	Lys	Arg	Gly	Cys	Gly	Ala	Ala	Arg	Arg	Gly	Pro	Arg
225					230					235					240
Ser	Trp	Thr	Cys	Gly	Cys	Trp	Gly	Gln	Phe	Glu	His	Tyr	Arg	Arg	Ala
				245					250					255	
Cys	Arg	Arg	Cys	Arg	Arg	Gly	Cys	Arg	Ala	Trp	Arg	Ala	Cys	Pro	Gly
			260					265					270		
Pro	Leu	Ser	Arg	Gly	Arg	Ser	Pro	Gly	Pro	Val	Leu	Gly	His	Gly	Pro
		275					280					285			
Leu	Gly	Ser	Arg	Gly	Pro	Arg	Cys	Ser	Ser	Ser	Ser	Cys	Gly	Pro	Ser
	290					295						300			
Ser	Ser	Ser	Gly	Ser	Ser	Glu	Cys	Phe	Gly	Pro	Lys	Arg	Gly	Asp	Cys
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Gln	Trp	Arg	Gly	Leu	Cys	Ser	Gln	Leu	Arg	Leu	Ser	Cys	Cys	Ala	Leu
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Ser	Leu	Pro	Arg	Val											
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (90)..(740)

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 Met Arg Leu Ser Ala Leu Leu Ala
 1 5

 ttg gca tcc aag gtc act ctg ccc ccc cat tac cgc tat ggg atg agc 161

Leu	Ala	Ser	Lys	Val	Thr	Leu	Pro	Pro	His	Tyr	Arg	Tyr	Gly	Met	Ser		
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ccc	cca	ggc	tct	gtt	gca	gac	aag	agg	aag	aac	ccc	cca	tgg	atc	agg	209	
Pro	Pro	Gly	Ser	Val	Ala	Asp	Lys	Arg	Lys	Asn	Pro	Pro	Trp	Ile	Arg		
25					30					35					40		
cgg	cgc	cca	gtg	gtt	gtg	gaa	ccc	atc	tct	gat	gaa	gac	tgg	tat	ctg	257	
Arg	Arg	Pro	Val	Val	Val	Glu	Pro	Ile	Ser	Asp	Glu	Asp	Trp	Tyr	Leu		
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ttc	tgt	ggg	gac	acg	gtg	gag	atc	cta	gaa	ggc	aag	gat	gcc	ggg	aag	305	
Phe	Cys	Gly	Asp	Thr	Val	Glu	Ile	Leu	Glu	Gly	Lys	Asp	Ala	Gly	Lys		
			60					65					70				
cag	ggc	aaa	gtg	gtt	caa	gtt	atc	cgg	cag	cga	aac	tgg	gtg	gtc	gtg	353	
Gln	Gly	Lys	Val	Val	Gln	Val	Ile	Arg	Gln	Arg	Asn	Trp	Val	Val	Val		
		75					80					85					
gga	ggg	ctg	aac	aca	cat	tac	cgc	tac	att	ggc	aag	acc	atg	gat	tac	401	
Gly	Gly	Leu	Asn	Thr	His	Tyr	Arg	Tyr	Ile	Gly	Lys	Thr	Met	Asp	Tyr		
	90					95					100						
cgg	gga	acc	atg	atc	cct	agt	gaa	gcc	ccc	ttg	ctc	cac	cgc	cag	gtc	449	
Arg	Gly	Thr	Met	Ile	Pro	Ser	Glu	Ala	Pro	Leu	Leu	His	Arg	Gln	Val		
105					110					115					120		
aaa	ctt	gtg	gat	cct	atg	gac	agg	aaa	ccc	act	gag	atc	gag	tgg	aga	497	
Lys	Leu	Val	Asp	Pro	Met	Asp	Arg	Lys	Pro	Thr	Glu	Ile	Glu	Trp	Arg		
				125					130					135			
ttt	act	gaa	gca	gga	gag	cgg	gta	cga	gtc	tcc	aca	cga	tca	ggg	aga	545	
Phe	Thr	Glu	Ala	Gly	Glu	Arg	Val	Arg	Val	Ser	Thr	Arg	Ser	Gly	Arg		
			140					145					150				
att	atc	cct	aaa	ccc	gaa	ttt	ccc	aga	gct	gat	ggc	atc	gtc	cct	gaa	593	
Ile	Ile	Pro	Lys	Pro	Glu	Phe	Pro	Arg	Ala	Asp	Gly	Ile	Val	Pro	Glu		
		155					160					165					
acg	tgg	att	gat	ggc	ccc	aaa	gac	aca	tca	gtg	gaa	gat	gct	tta	gaa	641	
Thr	Trp	Ile	Asp	Gly	Pro	Lys	Asp	Thr	Ser	Val	Glu	Asp	Ala	Leu	Glu		
	170					175					180						
aga	acc	tat	gtg	ccc	tgt	cta	aag	aca	ctg	cag	gag	gag	gtg	atg	gag	689	
Arg	Thr	Tyr	Val	Pro	Cys	Leu	Lys	Thr	Leu	Gln	Glu	Glu	Val	Met	Glu		
185					190					195					200		
gcc	atg	ggg	atc	aag	gag	acc	cgg	aaa	tac	aag	aag	gtc	tat	tgg	tat	737	
Ala	Met	Gly	Ile	Lys	Glu	Thr	Arg	Lys	Tyr	Lys	Lys	Val	Tyr	Trp	Tyr		
			205					210					215				
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<210> 146
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 146
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 35 40 45
 Ile Ser Asp Glu Asp Trp Tyr Leu Phe Cys Gly Asp Thr Val Glu Ile
 50 55 60
 Leu Glu Gly Lys Asp Ala Gly Lys Gln Gly Lys Val Val Gln Val Ile
 65 70 75 80
 Arg Gln Arg Asn Trp Val Val Val Gly Gly Leu Asn Thr His Tyr Arg
 85 90 95
 Tyr Ile Gly Lys Thr Met Asp Tyr Arg Gly Thr Met Ile Pro Ser Glu
 100 105 110
 Ala Pro Leu Leu His Arg Gln Val Lys Leu Val Asp Pro Met Asp Arg
 115 120 125
 Lys Pro Thr Glu Ile Glu Trp Arg Phe Thr Glu Ala Gly Glu Arg Val
 130 135 140
 Arg Val Ser Thr Arg Ser Gly Arg Ile Ile Pro Lys Pro Glu Phe Pro
 145 150 155 160
 Arg Ala Asp Gly Ile Val Pro Glu Thr Trp Ile Asp Gly Pro Lys Asp
 165 170 175
 Thr Ser Val Glu Asp Ala Leu Glu Arg Thr Tyr Val Pro Cys Leu Lys
 180 185 190
 Thr Leu Gln Glu Glu Val Met Glu Ala Met Gly Ile Lys Glu Thr Arg
 195 200 205
 Lys Tyr Lys Lys Val Tyr Trp Tyr
 210 215

<210> 147
 <211> 2465
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (71)..(1261)

<400> 147
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 Met Lys Ala Val Lys Ser Glu Arg Glu Arg Gly Ser Arg
 1 5 10
 cga aga cac cgg gac ggg gac gtg gtg ctg ccg gcg ggg gtg gtg gtg 157
 Arg Arg His Arg Asp Gly Asp Val Val Leu Pro Ala Gly Val Val Val
 15 20 25
 aag cag gag cgt ctc agc cca gaa gtc gca cct ccc gcc cac cgc cgt 205

Lys	Gln	Glu	Arg	Leu	Ser	Pro	Glu	Val	Ala	Pro	Pro	Ala	His	Arg	Arg	
30					35					40					45	
ccg	gac	cac	tcc	ggt	ggt	agc	ccg	tct	ccg	ccg	acc	agc	gag	ccg	gcc	253
Pro	Asp	His	Ser	Gly	Gly	Ser	Pro	Ser	Pro	Pro	Thr	Ser	Glu	Pro	Ala	
				50					55					60		
cgc	tcg	ggc	cac	cgc	ggg	aac	cga	gcc	cga	gga	gtt	agc	cgg	tcc	cca	301
Arg	Ser	Gly	His	Arg	Gly	Asn	Arg	Ala	Arg	Gly	Val	Ser	Arg	Ser	Pro	
			65					70					75			
ccc	aaa	aag	aaa	aac	aag	gcc	tca	ggg	aga	aga	agc	aag	tct	cct	cgc	349
Pro	Lys	Lys	Lys	Asn	Lys	Ala	Ser	Gly	Arg	Arg	Ser	Lys	Ser	Pro	Arg	
		80					85					90				
agt	aag	aga	aac	cga	agt	cct	cac	cac	tca	aca	gtc	aaa	gtg	aag	cag	397
Ser	Lys	Arg	Asn	Arg	Ser	Pro	His	His	Ser	Thr	Val	Lys	Val	Lys	Gln	
	95					100					105					
gag	cgt	gag	gat	cat	ccc	cgg	aga	gga	cgg	gag	gat	cgg	cag	cac	agg	445
Glu	Arg	Glu	Asp	His	Pro	Arg	Arg	Gly	Arg	Glu	Asp	Arg	Gln	His	Arg	
110					115					120					125	
gaa	cca	tca	gaa	cag	gaa	cac	agg	aga	gct	agg	aac	agt	gac	cgg	gac	493
Glu	Pro	Ser	Glu	Gln	Glu	His	Arg	Arg	Ala	Arg	Asn	Ser	Asp	Arg	Asp	
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aga	cac	cgg	ggc	cat	tcc	cac	caa	agg	aga	acg	tct	aac	gag	agg	cct	541
Arg	His	Arg	Gly	His	Ser	His	Gln	Arg	Arg	Thr	Ser	Asn	Glu	Arg	Pro	
			145					150					155			
ggg	agt	ggg	cag	ggt	cag	gga	cgg	gat	cga	gac	act	cag	aac	ctg	cag	589
Gly	Ser	Gly	Gln	Gly	Gln	Gly	Arg	Asp	Arg	Asp	Thr	Gln	Asn	Leu	Gln	
		160					165					170				
gct	cag	gaa	gaa	gag	cgg	gag	ttt	tat	aat	gcc	agg	cga	cgg	gag	cat	637
Ala	Gln	Glu	Glu	Glu	Arg	Glu	Phe	Tyr	Asn	Ala	Arg	Arg	Arg	Glu	His	
	175					180					185					
cgc	cag	agg	aat	gac	gtt	ggt	ggt	ggc	ggc	agt	gag	tct	cag	gag	ttg	685
Arg	Gln	Arg	Asn	Asp	Val	Gly	Gly	Gly	Gly	Ser	Glu	Ser	Gln	Glu	Leu	
190					195					200					205	
gtt	cct	cgg	cct	ggt	ggc	aac	aac	aaa	gaa	aaa	gag	gtg	ccc	gct	aaa	733
Val	Pro	Arg	Pro	Gly	Gly	Asn	Asn	Lys	Glu	Lys	Glu	Val	Pro	Ala	Lys	
				210					215					220		
gaa	aaa	cca	agc	ttt	gaa	ctt	tct	ggg	gca	ctt	ctt	gag	gac	acc	aac	781
Glu	Lys	Pro	Ser	Phe	Glu	Leu	Ser	Gly	Ala	Leu	Leu	Glu	Asp	Thr	Asn	
			225					230					235			
act	ttc	cgg	ggt	gta	gtc	att	aaa	tat	agt	gag	ccc	cca	gaa	gca	cgt	829
Thr	Phe	Arg	Gly	Val	Val	Ile	Lys	Tyr	Ser	Glu	Pro	Pro	Glu	Ala	Arg	
		240					245					250				
atc	ccc	aaa	aaa	cgg	tgg	cgt	ctc	tac	cca	ttt	aaa	aat	gat	gag	gtg	877
Ile	Pro	Lys	Lys	Arg	Trp	Arg	Leu	Tyr	Pro	Phe	Lys	Asn	Asp	Glu	Val	

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Leu Pro Val Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg			
270	275	280	285
cac cgc cgc att gca gac att cca att gat cac ccg tct tgt tca aag			973
His Arg Arg Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys			
290	295		300
cag cat gcg gtc ttt caa tat cgg ctt gtg gaa tat acc cgt gct gat			1021
Gln His Ala Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp			
305	310		315
ggc aca gtt ggc cga aga gtg aag ccc tac atc att gac ctt ggc tca			1069
Gly Thr Val Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser			
320	325		330
ggc aat gga acc ttc tta aac aac aaa cgt att gag cca cag aga tac			1117
Gly Asn Gly Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr			
335	340		345
tat gaa cta aaa gaa aag gat gta ctc aaa ttt gga ttc agt agc aga			1165
Tyr Glu Leu Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg			
350	355		360
gaa tac gtc ttg ctc cat gag tcg tcg gac act tct gaa ata gac agg			1213
Glu Tyr Val Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg			
370	375		380
aaa gat gac gag gat gag gag gag gag gaa gaa gtg tct gac agc tag			1261
Lys Asp Asp Glu Asp Glu Glu Glu Glu Glu Glu Val Ser Asp Ser			
385	390		395
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cagtgggtgc tgattcagca tcacaagtga ctgaaattgg ctgtggatct gttctttgtg 1981			

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 aattgtgtgt taaagagctg atactgattt tcatatgaca atgttaggca aaggcctccc 2401
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 atat 2465

<210> 148
 <211> 396
 <212> PRT
 <213> Homo sapiens

<400> 148

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			20					25					30		
Arg	Leu	Ser	Pro	Glu	Val	Ala	Pro	Pro	Ala	His	Arg	Arg	Pro	Asp	His
		35					40					45			
Ser	Gly	Gly	Ser	Pro	Ser	Pro	Pro	Thr	Ser	Glu	Pro	Ala	Arg	Ser	Gly
	50					55					60				
His	Arg	Gly	Asn	Arg	Ala	Arg	Gly	Val	Ser	Arg	Ser	Pro	Pro	Lys	Lys
	65				70					75					80
Lys	Asn	Lys	Ala	Ser	Gly	Arg	Arg	Ser	Lys	Ser	Pro	Arg	Ser	Lys	Arg
				85					90					95	
Asn	Arg	Ser	Pro	His	His	Ser	Thr	Val	Lys	Val	Lys	Gln	Glu	Arg	Glu
			100					105					110		
Asp	His	Pro	Arg	Arg	Gly	Arg	Glu	Asp	Arg	Gln	His	Arg	Glu	Pro	Ser
	115					120					125				
Glu	Gln	Glu	His	Arg	Arg	Ala	Arg	Asn	Ser	Asp	Arg	Asp	Arg	His	Arg
	130					135					140				
Gly	His	Ser	His	Gln	Arg	Arg	Thr	Ser	Asn	Glu	Arg	Pro	Gly	Ser	Gly
145				150						155					160
Gln	Gly	Gln	Gly	Arg	Asp	Arg	Asp	Thr	Gln	Asn	Leu	Gln	Ala	Gln	Glu
			165					170						175	
Glu	Glu	Arg	Glu	Phe	Tyr	Asn	Ala	Arg	Arg	Arg	Glu	His	Arg	Gln	Arg
			180				185						190		
Asn	Asp	Val	Gly	Gly	Gly	Gly	Ser	Glu	Ser	Gln	Glu	Leu	Val	Pro	Arg
	195					200						205			
Pro	Gly	Gly	Asn	Asn	Lys	Glu	Lys	Glu	Val	Pro	Ala	Lys	Glu	Lys	Pro
	210				215						220				
Ser	Phe	Glu	Leu	Ser	Gly	Ala	Leu	Leu	Glu	Asp	Thr	Asn	Thr	Phe	Arg
225					230					235					240
Gly	Val	Val	Ile	Lys	Tyr	Ser	Glu	Pro	Pro	Glu	Ala	Arg	Ile	Pro	Lys

75	80	85	
atc gag gag tgc aag cag gtg att ctg gag ctg ccc gag cag tcg gag Ile Glu Glu Cys Lys Gln Val Ile Leu Glu Leu Pro Glu Gln Ser Glu 90 95 100			460
aag cag aag gat gcc gtg gtg cga ctc atc cac ctc cgg ctg aag ctc Lys Gln Lys Asp Ala Val Val Arg Leu Ile His Leu Arg Leu Lys Leu 105 110 115 120			508
cag gag ctg aag gac ccc aat gag gat gag cca aac atc cga gtg ctc Gln Glu Leu Lys Asp Pro Asn Glu Asp Glu Pro Asn Ile Arg Val Leu 125 130 135			556
ctt gag cac cgc ttt tac aag gag aag agc aag agc gtc aag cag acc Leu Glu His Arg Phe Tyr Lys Glu Lys Ser Lys Ser Val Lys Gln Thr 140 145 150			604
tgt gac aag tgt aac acc atc atc tgg ggg ctc att cag acc tgg tac Cys Asp Lys Cys Asn Thr Ile Ile Trp Gly Leu Ile Gln Thr Trp Tyr 155 160 165			652
acc tgc aca ggg tgt tat tac cgc tgt cac agt aag tgc ttg aac ctc Thr Cys Thr Gly Cys Tyr Tyr Arg Cys His Ser Lys Cys Leu Asn Leu 170 175 180			700
atc tcc aag ccc tgt gtg agc tcc aaa gtc agc cac caa gct gaa tac Ile Ser Lys Pro Cys Val Ser Ser Lys Val Ser His Gln Ala Glu Tyr 185 190 195 200			748
gaa ctg aac atc tgc cct gag aca ggg ctg gac agc cag gat tac cgc Glu Leu Asn Ile Cys Pro Glu Thr Gly Leu Asp Ser Gln Asp Tyr Arg 205 210 215			796
tgt gcc gag tgc cgg gcg ccc atc tct ctg cgg ggt gtg ccc agt gag Cys Ala Glu Cys Arg Ala Pro Ile Ser Leu Arg Gly Val Pro Ser Glu 220 225 230			844
gcc agg cag tgc gac tac acc ggc cag tac tac tgc agc cac tgc cac Ala Arg Gln Cys Asp Tyr Thr Gly Gln Tyr Tyr Cys Ser His Cys His 235 240 245			892
tgg aac gac ctg gct gtg atc cct gca cgc gtt gta cac aac tgg gac Trp Asn Asp Leu Ala Val Ile Pro Ala Arg Val Val His Asn Trp Asp 250 255 260			940
ttt gag cct cga aag gtt tct cgc tgc agc atg cgc tac ctg gcg ctg Phe Glu Pro Arg Lys Val Ser Arg Cys Ser Met Arg Tyr Leu Ala Leu 265 270 275 280			988
atg gtg tct cgg ccc gta ctc agg ctc cgg gag atc aac cct ctg ctg Met Val Ser Arg Pro Val Leu Arg Leu Arg Glu Ile Asn Pro Leu Leu 285 290 295			1036
ttc agc tac gtg gag gag ctg gtg gag att cgc aag ctg cgc cag gac Phe Ser Tyr Val Glu Glu Leu Val Glu Ile Arg Lys Leu Arg Gln Asp 300 305 310			1084

atc ctg ctc atg aag ccg tac ttc atc acc tgc agg gag gcc atg gag	1132
Ile Leu Leu Met Lys Pro Tyr Phe Ile Thr Cys Arg Glu Ala Met Glu	
315 320 325	
gct cgt ctg ctg ctg cag ctc cag gat cgg cag cat ttt gtg gag aac	1180
Ala Arg Leu Leu Leu Gln Leu Gln Asp Arg Gln His Phe Val Glu Asn	
330 335 340	
gac gag atg tac tct gtc cag gac ctc ctg gac gtg cat gcc ggc cgc	1228
Asp Glu Met Tyr Ser Val Gln Asp Leu Leu Asp Val His Ala Gly Arg	
345 350 355 360	
ctg ggc tgc tgc ctc acc gag atc cac acg ctc ttc gcc aag cac atc	1276
Leu Gly Cys Ser Leu Thr Glu Ile His Thr Leu Phe Ala Lys His Ile	
365 370 375	
aag ctg gac tgc gag cgg tgc cag gcc aag ggc ttc gtg tgt gag ctc	1324
Lys Leu Asp Cys Glu Arg Cys Gln Ala Lys Gly Phe Val Cys Glu Leu	
380 385 390	
tgc aga gag ggc gac gtg ctg ttc ccg ttc gac agc cac acg tct gtg	1372
Cys Arg Glu Gly Asp Val Leu Phe Pro Phe Asp Ser His Thr Ser Val	
395 400 405	
tgc gcc gac tgc tcc gcg gtc ttc cac agg gac tgc tac tac gac aac	1420
Cys Ala Asp Cys Ser Ala Val Phe His Arg Asp Cys Tyr Tyr Asp Asn	
410 415 420	
tcc acc act tgt ccc aag tgt gcc cgg ctc agc ctg agg aag cag tgc	1468
Ser Thr Thr Cys Pro Lys Cys Ala Arg Leu Ser Leu Arg Lys Gln Ser	
425 430 435 440	
ctc ttc cag gag cca ggt ccc gat gtg gag gcc tag cgccgaggaa	1514
Leu Phe Gln Glu Pro Gly Pro Asp Val Glu Ala	
445 450	
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gtcctgtttc cccttctct ttggggctga ggaggaggtt aaaggccaaa tgctgtttcc 3194
caacacccca aagtctgcac acgtctcatg aatgcatcac atttctgtca tatggatatt 3254
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tatggttctt tctgtgggtc tgtggcacag caggaagagc ccggtgccgc cagcaccttg 3494
tggaagacca cacatgggtg gtcccacagc atgggaccag gctggcctga gggatgccca 3554
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<210> 150
<211> 451
<212> PRT
<213> Homo sapiens
<400> 150

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Pro	Phe	Asn	Lys	Gln	Ser	Gly	Pro	Arg	Gln	His	Glu	Gln	Gly	Pro	Gly
			20					25					30		
Glu	Glu	Val	Pro	Asp	Val	Thr	Pro	Glu	Glu	Ala	Leu	Pro	Glu	Leu	Pro
		35					40					45			
Pro	Gly	Glu	Pro	Glu	Phe	Arg	Cys	Pro	Glu	Arg	Val	Met	Asp	Leu	Gly
	50					55					60				
Leu	Ser	Glu	Asp	His	Phe	Ser	Arg	Pro	Val	Gly	Leu	Phe	Leu	Ala	Ser
65					70					75					80
Asp	Val	Gln	Gln	Leu	Arg	Gln	Ala	Ile	Glu	Glu	Cys	Lys	Gln	Val	Ile
				85					90					95	
Leu	Glu	Leu	Pro	Glu	Gln	Ser	Glu	Lys	Gln	Lys	Asp	Ala	Val	Val	Arg
			100					105					110		
Leu	Ile	His	Leu	Arg	Leu	Lys	Leu	Gln	Glu	Leu	Lys	Asp	Pro	Asn	Glu
	115						120					125			
Asp	Glu	Pro	Asn	Ile	Arg	Val	Leu	Leu	Glu	His	Arg	Phe	Tyr	Lys	Glu
130						135					140				
Lys	Ser	Lys	Ser	Val	Lys	Gln	Thr	Cys	Asp	Lys	Cys	Asn	Thr	Ile	Ile
145					150					155					160
Trp	Gly	Leu	Ile	Gln	Thr	Trp	Tyr	Thr	Cys	Thr	Gly	Cys	Tyr	Tyr	Arg
				165					170					175	
Cys	His	Ser	Lys	Cys	Leu	Asn	Leu	Ile	Ser	Lys	Pro	Cys	Val	Ser	Ser
			180					185					190		
Lys	Val	Ser	His	Gln	Ala	Glu	Tyr	Glu	Leu	Asn	Ile	Cys	Pro	Glu	Thr
	195						200					205			
Gly	Leu	Asp	Ser	Gln	Asp	Tyr	Arg	Cys	Ala	Glu	Cys	Arg	Ala	Pro	Ile
210						215					220				
Ser	Leu	Arg	Gly	Val	Pro	Ser	Glu	Ala	Arg	Gln	Cys	Asp	Tyr	Thr	Gly
225					230					235					240
Gln	Tyr	Tyr	Cys	Ser	His	Cys	His	Trp	Asn	Asp	Leu	Ala	Val	Ile	Pro
				245					250					255	
Ala	Arg	Val	Val	His	Asn	Trp	Asp	Phe	Glu	Pro	Arg	Lys	Val	Ser	Arg
			260					265					270		
Cys	Ser	Met	Arg	Tyr	Leu	Ala	Leu	Met	Val	Ser	Arg	Pro	Val	Leu	Arg
		275					280					285			
Leu	Arg	Glu	Ile	Asn	Pro	Leu	Leu	Phe	Ser	Tyr	Val	Glu	Glu	Leu	Val
290						295					300				
Glu	Ile	Arg	Lys	Leu	Arg	Gln	Asp	Ile	Leu	Leu	Met	Lys	Pro	Tyr	Phe
305					310					315					320
Ile	Thr	Cys	Arg	Glu	Ala	Met	Glu	Ala	Arg	Leu	Leu	Leu	Gln	Leu	Gln
				325					330					335	
Asp	Arg	Gln	His	Phe	Val	Glu	Asn	Asp	Glu	Met	Tyr	Ser	Val	Gln	Asp
			340					345					350		
Leu	Leu	Asp	Val	His	Ala	Gly	Arg	Leu	Gly	Cys	Ser	Leu	Thr	Glu	Ile
		355					360					365			
His	Thr	Leu	Phe	Ala	Lys	His	Ile	Lys	Leu	Asp	Cys	Glu	Arg	Cys	Gln
370						375					380				
Ala	Lys	Gly	Phe	Val	Cys	Glu	Leu	Cys	Arg	Glu	Gly	Asp	Val	Leu	Phe
385					390					395					400
Pro	Phe	Asp	Ser	His	Thr	Ser	Val	Cys	Ala	Asp	Cys	Ser	Ala	Val	Phe
				405					410					415	
His	Arg	Asp	Cys	Tyr	Tyr	Asp	Asn	Ser	Thr	Thr	Cys	Pro	Lys	Cys	Ala
			420				425					430			
Arg	Leu	Ser	Leu	Arg	Lys	Gln	Ser	Leu	Phe	Gln	Glu	Pro	Gly	Pro	Asp
		435					440					445			
Val	Glu	Ala													

450

<210> 151
 <211> 442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (12)..(353)

<400> 151
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 Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly Ala
 1 5 10

ttg tcc gga gct gcg gcc tta ggc ttc gct tcc tac ggg gcg cac ggc 98
 Leu Ser Gly Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly
 15 20 25

gcc caa ttc cca gat gcc tac ggg aag gag ctg ttt gac aag gcc aac 146
 Ala Gln Phe Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala Asn
 30 35 40 45

aaa cac cac ttc tta cac agc ctg gcc ctg tta ggg gtg ccc cat tgc 194
 Lys His His Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His Cys
 50 55 60

aga aag cca ctc tgg gct ggg tta ttg cta gct tcc gga acg acc tta 242
 Arg Lys Pro Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr Leu
 65 70 75

ttc tgc acc agc ttt tac tac cag gct ctg agt gga gac ccc agc atc 290
 Phe Cys Thr Ser Phe Tyr Tyr Gln Ala Leu Ser Gly Asp Pro Ser Ile
 80 85 90

cag act ttg gcc cct gcg gga ggg acc ctg cta ctc ttg ggc tgg ctt 338
 Gln Thr Leu Ala Pro Ala Gly Gly Thr Leu Leu Leu Leu Gly Trp Leu
 95 100 105

gcc ttg gct ctt tga gctccctttt gcttaattac tgggttttct gggcagtttt 393
 Ala Leu Ala Leu
 110

tttttttaaa gagttggagt aagaagagga ttaaaaagga aaggcaaatt 442

<210> 152
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 152
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 1 5 10 15
 Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His Gly Ala Gln Phe

Ala	Lys	Met	Pro	Gln	Met	Ile	Val	Asn	Trp	Gln	Gln	Gln	Gln	Arg	Glu	
				130					135						140	
aac	tgg	gag	aag	gcc	cag	gct	gac	aag	gag	agg	agg	gcc	cga	ctg	cag	482
Asn	Trp	Glu	Lys	Ala	Gln	Ala	Asp	Lys	Glu	Arg	Arg	Ala	Arg	Leu	Gln	
			145					150					155			
gct	gag	gcc	cag	gag	ctc	ctg	ggc	tac	cag	gtg	gac	cca	agg	agt	gcc	530
Ala	Glu	Ala	Gln	Glu	Leu	Leu	Gly	Tyr	Gln	Val	Asp	Pro	Arg	Ser	Ala	
		160					165					170				
cgc	ttc	cag	gag	ctg	ctc	cag	gac	cta	gag	aag	aag	gag	cgc	aag	cgc	578
Arg	Phe	Gln	Glu	Leu	Leu	Gln	Asp	Leu	Glu	Lys	Lys	Glu	Arg	Lys	Arg	
	175					180					185					
ctc	aag	gag	gaa	aaa	cag	aaa	cgg	aag	aag	gag	gcg	cga	gct	gct	gca	626
Leu	Lys	Glu	Glu	Lys	Gln	Lys	Arg	Lys	Lys	Glu	Ala	Arg	Ala	Ala	Ala	
190					195					200					205	
ttg	gct	gca	gct	gtg	gct	caa	gac	cca	gca	gcc	tct	ggg	gca	ccc	agc	674
Leu	Ala	Ala	Ala	Val	Ala	Gln	Asp	Pro	Ala	Ala	Ser	Gly	Ala	Pro	Ser	
				210					215					220		
tcc	tga	ggctttgtcc	cttcccaata	aagcctgcta	cctggcagta	cccctg										726
Ser																

<210> 154
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 154

Met	Ala	Ala	Ser	Val	Arg	Gln	Ala	Arg	Ser	Leu	Leu	Gly	Val	Ala	Ala	
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Thr	Leu	Ala	Pro	Gly	Ser	Arg	Gly	Tyr	Arg	Ala	Arg	Pro	Pro	Pro	Arg	
			20					25					30			
Arg	Arg	Pro	Gly	Pro	Arg	Trp	Pro	Asp	Pro	Glu	Asp	Leu	Leu	Thr	Pro	
		35					40					45				
Arg	Trp	Gln	Leu	Gly	Pro	Arg	Tyr	Ala	Ala	Lys	Gln	Phe	Ala	Arg	Tyr	
	50					55					60					
Gly	Ala	Ala	Ser	Gly	Val	Val	Pro	Gly	Ser	Leu	Trp	Pro	Ser	Pro	Glu	
65					70					75					80	
Gln	Leu	Arg	Glu	Leu	Glu	Ala	Glu	Glu	Arg	Glu	Trp	Tyr	Pro	Ser	Leu	
			85					90						95		
Ala	Thr	Met	Gln	Glu	Ser	Leu	Arg	Val	Lys	Gln	Leu	Ala	Glu	Glu	Gln	
		100						105					110			
Lys	Arg	Arg	Glu	Arg	Glu	Gln	His	Ile	Ala	Glu	Cys	Met	Ala	Lys	Met	
	115						120					125				
Pro	Gln	Met	Ile	Val	Asn	Trp	Gln	Gln	Gln	Gln	Arg	Glu	Asn	Trp	Glu	
	130					135						140				
Lys	Ala	Gln	Ala	Asp	Lys	Glu	Arg	Arg	Ala	Arg	Leu	Gln	Ala	Glu	Ala	
145					150					155					160	
Gln	Glu	Leu	Leu	Gly	Tyr	Gln	Val	Asp	Pro	Arg	Ser	Ala	Arg	Phe	Gln	
				165					170					175		
Glu	Leu	Leu	Gln	Asp	Leu	Glu	Lys	Lys	Glu	Arg	Lys	Arg	Leu	Lys	Glu	
			180					185					190			

Glu Lys Gln Lys Arg Lys Lys Glu Ala Arg Ala Ala Ala Leu Ala Ala
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 Ala Val Ala Gln Asp Pro Ala Ala Ser Gly Ala Pro Ser Ser
 210 215 220

<210> 155
 <211> 1120
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (208)..(1044)

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 gccgaggcct gggttacaag cagcaagtgc gcggttgggg ccactgagag gccgttttag 180
 aaaactgttt aaaacaaaga gcaattg atg gat aaa tca gga ata gat tct ctt 234
 Met Asp Lys Ser Gly Ile Asp Ser Leu
 1 5
 gac cat gtg aca tct gat gct gtg gaa ctt gca aat cga agt gat aac 282
 Asp His Val Thr Ser Asp Ala Val Glu Leu Ala Asn Arg Ser Asp Asn
 10 15 20 25
 tct tct gat agc agc tta ttt aaa act cag tgt atc cct tac tca cct 330
 Ser Ser Asp Ser Ser Leu Phe Lys Thr Gln Cys Ile Pro Tyr Ser Pro
 30 35 40
 aaa ggg gag aaa aga aac ccc att cga aaa ttt gtt cgt aca cct gaa 378
 Lys Gly Glu Lys Arg Asn Pro Ile Arg Lys Phe Val Arg Thr Pro Glu
 45 50 55
 agt gtt cac gca agt gat tca tca agt gac tca tct ttt gaa cca ata 426
 Ser Val His Ala Ser Asp Ser Ser Ser Asp Ser Ser Phe Glu Pro Ile
 60 65 70
 cca ttg act ata aaa gct att ttt gaa aga ttc aag aac agg aaa aag 474
 Pro Leu Thr Ile Lys Ala Ile Phe Glu Arg Phe Lys Asn Arg Lys Lys
 75 80 85
 aga tat aaa aaa aag aaa aag agg agg tac cag cca aca gga aga cca 522
 Arg Tyr Lys Lys Lys Lys Lys Arg Arg Tyr Gln Pro Thr Gly Arg Pro
 90 95 100 105
 cgg gga aga cca gaa gga agg aga aat cct ata tac tca cta ata gat 570
 Arg Gly Arg Pro Glu Gly Arg Arg Asn Pro Ile Tyr Ser Leu Ile Asp
 110 115 120
 aag aag aaa caa ttt aga agc aga gga tct ggc ttc cca ttt tta gaa 618
 Lys Lys Lys Gln Phe Arg Ser Arg Gly Ser Gly Phe Pro Phe Leu Glu
 125 130 135

65 70 75 80
Phe Glu Arg Phe Lys Asn Arg Lys Lys Arg Tyr Lys Lys Lys Lys Lys
85 90 95
Arg Arg Tyr Gln Pro Thr Gly Arg Pro Arg Gly Arg Pro Glu Gly Arg
100 105 110
Arg Asn Pro Ile Tyr Ser Leu Ile Asp Lys Lys Lys Gln Phe Arg Ser
115 120 125
Arg Gly Ser Gly Phe Pro Phe Leu Glu Ser Glu Asn Glu Lys Asn Ala
130 135 140
Pro Trp Arg Lys Ile Leu Thr Phe Glu Gln Ala Val Ala Arg Gly Phe
145 150 155 160
Phe Asn Tyr Ile Glu Lys Leu Lys Tyr Glu His His Leu Lys Glu Ser
165 170 175
Leu Lys Gln Met Asn Val Gly Glu Asp Leu Glu Asn Glu Asp Phe Asp
180 185 190
Ser Arg Arg Tyr Lys Phe Leu Asp Asp Asp Gly Ser Ile Ser Pro Ile
195 200 205
Glu Glu Ser Thr Ala Glu Asp Glu Asp Ala Thr His Leu Glu Asp Asn
210 215 220
Glu Cys Asp Ile Lys Leu Ala Gly Asp Ser Phe Ile Val Ser Ser Glu
225 230 235 240
Phe Pro Val Arg Leu Ser Val Tyr Leu Glu Glu Glu Asp Ile Thr Glu
245 250 255
Glu Ala Ala Leu Ser Lys Lys Arg Ala Thr Lys Ala Lys Asn Thr Gly
260 265 270
Gln Arg Gly Leu Lys Met
275

<210> 157
<211> 747
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (27)..(692)

<400> 157
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Met Ala Gly Thr Gly Leu Leu Ala Leu
1 5

cgg acg ctg cca ggg ccc agc tgg gtg cga ggc tcg ggc cct tcc gtg 101
Arg Thr Leu Pro Gly Pro Ser Trp Val Arg Gly Ser Gly Pro Ser Val
10 15 20 25

ctg agc cgc ctg cag gac gcg gcc gtg gtg cgg cct ggc ttc ctg agc 149
Leu Ser Arg Leu Gln Asp Ala Ala Val Val Arg Pro Gly Phe Leu Ser
30 35 40

acg gca gag gag gag acg ctg agc cga gaa ctg gag ccc gag ctg cgc 197
Thr Ala Glu Glu Glu Thr Leu Ser Arg Glu Leu Glu Pro Glu Leu Arg
45 50 55

cgc cgc cgc tac gaa tac gat cac tgg gac gcg gcc atc cac ggc ttc 245
Arg Arg Arg Tyr Glu Tyr Asp His Trp Asp Ala Ala Ile His Gly Phe

60	65	70	
cga gag aca gag aag tcg cgc tgg tca gaa gcc agc cgg gcc atc ctg			293
Arg Glu Thr Glu Lys Ser Arg Trp Ser Glu Ala Ser Arg Ala Ile Leu			
75	80	85	
cag cgc gtg cag gcg gcc gcc ttt ggc ccc ggc cag acc ctg ctc tcc			341
Gln Arg Val Gln Ala Ala Ala Phe Gly Pro Gly Gln Thr Leu Leu Ser			
90	95	100	105
tcc gtg cac gtg ctg gac ctg gaa gcc cgc ggc tac atc aag ccc cac			389
Ser Val His Val Leu Asp Leu Glu Ala Arg Gly Tyr Ile Lys Pro His			
110	115	120	
gtg gac agc atc aag ttc tgc ggg gcc acc atc gcc ggc ctg tct ctc			437
Val Asp Ser Ile Lys Phe Cys Gly Ala Thr Ile Ala Gly Leu Ser Leu			
125	130	135	
ctg tct ccc agc gtt atg cgg ctg gtg cac acc cag gag ccg ggg gag			485
Leu Ser Pro Ser Val Met Arg Leu Val His Thr Gln Glu Pro Gly Glu			
140	145	150	
tgg ctg gaa ctc ttg ctg gag ccg ggc tcc ctc tac atc ctt agg ggc			533
Trp Leu Glu Leu Leu Leu Glu Pro Gly Ser Leu Tyr Ile Leu Arg Gly			
155	160	165	
tca gcc cgt tat gac ttc tcc cat gag atc ctt cgg gat gaa gag tcc			581
Ser Ala Arg Tyr Asp Phe Ser His Glu Ile Leu Arg Asp Glu Glu Ser			
170	175	180	185
ttc ttt ggg gaa cgc cgg att ccc cgg ggc cgg cgc atc tcc gtg atc			629
Phe Phe Gly Glu Arg Arg Ile Pro Arg Gly Arg Arg Ile Ser Val Ile			
190	195	200	
tgc cgc tcc ctc cct gag ggc atg ggg cca ggg gag tct gga cag ccg			677
Cys Arg Ser Leu Pro Glu Gly Met Gly Pro Gly Glu Ser Gly Gln Pro			
205	210	215	
ccc cca gcc tgc tga ccccccagctt tctacagaca ccagatttgt gaataaagtt			732
Pro Pro Ala Cys			
220			
ggggaatgga cagcc			747
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<211> 221			
<212> PRT			
<213> Homo sapiens			
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Met Ala Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser			
1	5	10	15
Trp Val Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala			
20	25	30	
Ala Val Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu			
35	40	45	

Gly	Pro	Thr	Ser	Gln	Asp	Thr	Ile	Arg	Asn	Gln	Val	Arg	Lys	Glu	Leu	
			75					80					85			
caa	gcc	gaa	gcc	acc	gtc	agc	ggg	agc	ccc	gag	gcc	cca	ggg	acc	aac	403
Gln	Ala	Glu	Ala	Thr	Val	Ser	Gly	Ser	Pro	Glu	Ala	Pro	Gly	Thr	Asn	
		90					95					100				
gtg	gta	tct	gag	ccc	aga	gag	gaa	ggc	tct	gcc	cac	ctg	gct	gtg	cct	451
Val	Val	Ser	Glu	Pro	Arg	Glu	Glu	Gly	Ser	Ala	His	Leu	Ala	Val	Pro	
	105					110					115					
ggc	gtg	tac	ttc	acc	tgt	ccg	ctc	act	ggg	gcc	acc	ctg	agg	aag	gac	499
Gly	Val	Tyr	Phe	Thr	Cys	Pro	Leu	Thr	Gly	Ala	Thr	Leu	Arg	Lys	Asp	
120					125					130					135	
cag	cgg	gac	gcc	tgc	atc	aag	gag	gcc	att	ctc	ttg	cac	ttc	tcc	acc	547
Gln	Arg	Asp	Ala	Cys	Ile	Lys	Glu	Ala	Ile	Leu	Leu	His	Phe	Ser	Thr	
			140						145					150		
gac	cca	gtg	gcc	gcc	tcc	atc	atg	aag	atc	tac	acg	ttc	aac	aaa	gac	595
Asp	Pro	Val	Ala	Ala	Ser	Ile	Met	Lys	Ile	Tyr	Thr	Phe	Asn	Lys	Asp	
			155					160					165			
cag	gac	cgg	gtg	aag	ctg	ggt	gtg	gac	acc	att	gcc	aag	tac	ctg	gac	643
Gln	Asp	Arg	Val	Lys	Leu	Gly	Val	Asp	Thr	Ile	Ala	Lys	Tyr	Leu	Asp	
		170					175					180				
aac	atc	cac	ctg	cac	ccc	gag	gag	gag	aag	tac	cgg	aag	atc	aag	ctg	691
Asn	Ile	His	Leu	His	Pro	Glu	Glu	Glu	Lys	Tyr	Arg	Lys	Ile	Lys	Leu	
	185					190					195					
cag	aac	aag	gtg	ttt	cag	gag	cgc	att	aac	tgc	ctg	gaa	ggg	acc	cac	739
Gln	Asn	Lys	Val	Phe	Gln	Glu	Arg	Ile	Asn	Cys	Leu	Glu	Gly	Thr	His	
200					205					210					215	
gag	ttt	ttt	gag	gcc	att	ggg	ttc	cag	aag	gtg	ttg	ctt	ccc	gcc	cag	787
Glu	Phe	Phe	Glu	Ala	Ile	Gly	Phe	Gln	Lys	Val	Leu	Leu	Pro	Ala	Gln	
			220						225					230		
gat	cag	gag	gac	ccc	gag	gag	ttc	tac	gtg	ctg	agc	gag	acc	acc	ttg	835
Asp	Gln	Glu	Asp	Pro	Glu	Glu	Phe	Tyr	Val	Leu	Ser	Glu	Thr	Thr	Leu	
			235					240					245			
gcc	cag	ccc	cag	agc	ctg	gag	agg	cac	aag	gaa	cag	ctg	ctg	gct	gcg	883
Ala	Gln	Pro	Gln	Ser	Leu	Glu	Arg	His	Lys	Glu	Gln	Leu	Leu	Ala	Ala	
		250					255					260				
gag	ccc	gtg	cgc	gcc	aag	ctg	gac	agg	cag	cgc	cgc	gtc	ttc	cag	ccc	931
Glu	Pro	Val	Arg	Ala	Lys	Leu	Asp	Arg	Gln	Arg	Arg	Val	Phe	Gln	Pro	
	265					270					275					
tcg	ccc	ctg	gcc	tcg	cag	ttc	gaa									

300	305	310	
gag cgg ctg agc gtg ctg cgg acc aag gcc atg cgg gag aag gag gag Glu Arg Leu Ser Val Leu Arg Thr Lys Ala Met Arg Glu Lys Glu Glu 315 320 325			1075
cag cgg ggg ctg cgc aag tac aac tac acg ctg ctg cgc gtg cgc ctc Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr Leu Leu Arg Val Arg Leu 330 335 340			1123
ccc gat ggc tgc ctc ctg cag ggc act ttc tac gct cgg gag cgg ctg Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe Tyr Ala Arg Glu Arg Leu 345 350 355			1171
ggg gcg gtg tac ggg ttc gtc cgg gag gcc ctg cag agc gac tgg ctg Gly Ala Val Tyr Gly Phe Val Arg Glu Ala Leu Gln Ser Asp Trp Leu 360 365 370 375			1219
cct ttt gag ctg ctg gcc tcg gga ggg cag aag ctg tcc gag gac gag Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys Leu Ser Glu Asp Glu 380 385 390			1267
aac ctg gcc ttg aac gag tgc ggg ctg gtg ccc tct gcc ctc ctg acc Asn Leu Ala Leu Asn Glu Cys Gly Leu Val Pro Ser Ala Leu Leu Thr 395 400 405			1315
ttc tcg tgg gac atg gct gtg ctg gag gac atc aag gcc gcg ggg gcc Phe Ser Trp Asp Met Ala Val Leu Glu Asp Ile Lys Ala Ala Gly Ala 410 415 420			1363
gag ccg gac tcc atc ctg aaa ccc gag ctc ctg tca gcc atc gag aag Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu Leu Ser Ala Ile Glu Lys 425 430 435			1411
ctc ttg tga aataaaaagca gggttggcct c Leu Leu 440			1441

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 <211> 441
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Lys Lys Phe Phe Gln Glu Phe Lys Ala Asp Ile Lys Phe Lys Ser
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 Ala Gly Pro Gly Gln Lys Leu Lys Glu Ser Val Gly Glu Lys Ala His
 20 25 30
 Lys Glu Lys Pro Asn Gln Pro Ala Pro Arg Pro Pro Arg Gln Gly Pro
 35 40 45
 Thr Asn Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu
 50 55 60
 Gln Lys Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg
 65 70 75 80
 Asn Gln Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser
 85 90 95

Pro	Glu	Ala	Pro	Gly	Thr	Asn	Val	Val	Ser	Glu	Pro	Arg	Glu	Glu	Gly	100	105	110
Ser	Ala	His	Leu	Ala	Val	Pro	Gly	Val	Tyr	Phe	Thr	Cys	Pro	Leu	Thr	115	120	125
Gly	Ala	Thr	Leu	Arg	Lys	Asp	Gln	Arg	Asp	Ala	Cys	Ile	Lys	Glu	Ala	130	135	140
Ile	Leu	Leu	His	Phe	Ser	Thr	Asp	Pro	Val	Ala	Ala	Ser	Ile	Met	Lys	145	150	155
Ile	Tyr	Thr	Phe	Asn	Lys	Asp	Gln	Asp	Arg	Val	Lys	Leu	Gly	Val	Asp	165	170	175
Thr	Ile	Ala	Lys	Tyr	Leu	Asp	Asn	Ile	His	Leu	His	Pro	Glu	Glu	Glu	180	185	190
Lys	Tyr	Arg	Lys	Ile	Lys	Leu	Gln	Asn	Lys	Val	Phe	Gln	Glu	Arg	Ile	195	200	205
Asn	Cys	Leu	Glu	Gly	Thr	His	Glu	Phe	Phe	Glu	Ala	Ile	Gly	Phe	Gln	210	215	220
Lys	Val	Leu	Leu	Pro	Ala	Gln	Asp	Gln	Glu	Asp	Pro	Glu	Glu	Phe	Tyr	225	230	235
Val	Leu	Ser	Glu	Thr	Thr	Leu	Ala	Gln	Pro	Gln	Ser	Leu	Glu	Arg	His	245	250	255
Lys	Glu	Gln	Leu	Leu	Ala	Ala	Glu	Pro	Val	Arg	Ala	Lys	Leu	Asp	Arg	260	265	270
Gln	Arg	Arg	Val	Phe	Gln	Pro	Ser	Pro	Leu	Ala	Ser	Gln	Phe	Glu	Leu	275	280	285
Pro	Gly	Asp	Phe	Phe	Asn	Leu	Thr	Ala	Glu	Glu	Ile	Lys	Arg	Glu	Gln	290	295	300
Arg	Leu	Arg	Ser	Glu	Ala	Val	Glu	Arg	Leu	Ser	Val	Leu	Arg	Thr	Lys	305	310	315
Ala	Met	Arg	Glu	Lys	Glu	Glu	Gln	Arg	Gly	Leu	Arg	Lys	Tyr	Asn	Tyr	325	330	335
Thr	Leu	Leu	Arg	Val	Arg	Leu	Pro	Asp	Gly	Cys	Leu	Leu	Gln	Gly	Thr	340	345	350
Phe	Tyr	Ala	Arg	Glu	Arg	Leu	Gly	Ala	Val	Tyr	Gly	Phe	Val	Arg	Glu	355	360	365
Ala	Leu	Gln	Ser	Asp	Trp	Leu	Pro	Phe	Glu	Leu	Leu	Ala	Ser	Gly	Gly	370	375	380
Gln	Lys	Leu	Ser	Glu	Asp	Glu	Asn	Leu	Ala	Leu	Asn	Glu	Cys	Gly	Leu	385	390	395
Val	Pro	Ser	Ala	Leu	Leu	Thr	Phe	Ser	Trp	Asp	Met	Ala	Val	Leu	Glu	405	410	415
Asp	Ile	Lys	Ala	Ala	Gly	Ala	Glu	Pro	Asp	Ser	Ile	Leu	Lys	Pro	Glu	420	425	430
Leu	Leu	Ser	Ala	Ile	Glu	Lys	Leu	Leu								435	440	